

GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: May 10, 2003, 15:59:43 ; Search time 1229 Seconds
(without alignments)
7104.021 Million cell updates/seq

Title: US-09-721-391-1

Perfect score: 300

Sequence: 1 tcatttgcaaggtcaaatca.....agccaagacatgtgataatc 300

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: gb_ba.*

2: gb_hgt.*

3: gb_in.*

4: gb_on.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vl.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_on.*

21: em_or.*

22: em_ov.*

23: em_pat.*

24: em_ph.*

25: em_pl.*

26: em_ro.*

27: em_sts.*

28: em_un.*

29: em_vl.*

30: em_htg_hum.*

31: em_htg_inv.*

32: em_htg_other.*

33: em_htg_mus.*

34: em_htg_pln.*

35: em_htg_rod.*

36: em_htg_mam.*

37: em_htg_vrt.*

38: em_sy.*

39: em_htgo_hum.*

40: em_htgo_mus.*

41: em_htgo_other.*

Pred. No. is the number of results predicted by chagne to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	300	100.0	300	6	AX269131	Sequence
2	300	100.0	1629	9	HUMTYR01	AK3235 Human tyros
3	300	100.0	2384	6	AR167367	AF167367 Sequence
4	300	100.0	2384	6	E11466	AF1466 cDNA encodi
5	300	100.0	2384	6	I49609	I49609 Sequence 1
6	300	100.0	2384	9	HUMTYR01	M21760 Human tyros
7	300	100.0	3586	9	HSTYR01E	X16073 Human tyros
8	300	100.0	147357	9	AP000720	AP000720 Homo sapi
9	293.6	97.9	1563	9	PAPATYR1	AF183649 Pan panis
10	292	97.3	1563	9	PPTYR1	AF183588 Pan trogl
11	289	96.3	2311	9	HS005039	U03039 Human tyros
12	289	96.3	2397	6	I70158	I70158 Sequence 11
13	287.2	95.7	1557	9	MNTYR1	AF183578 Macaca ne
14	287.2	95.7	1558	9	COPOTYR1	AF183593 Colobus p
15	287.2	95.7	1558	9	MATYR1	AF183614 Macaca ar
16	287.2	95.7	1558	9	MAASTYR1	AF183619 Macaca as
17	287.2	95.7	1559	9	MAFATYR1	AF183624 Macaca fa
18	287.2	95.7	1560	9	MAMUTYR1	AF183629 Macaca mu
19	287.2	95.7	1560	9	MTYR1	AF183659 Macaca th
20	285.6	95.2	1441	9	PHTYR1	AF183583 Papio ham
21	285.6	95.2	1556	9	PNTYR1	AF183654 Pygathrix
22	274.2	91.4	1562	9	RRTYR1	AF183669 Rhinopith
23	272.8	90.9	1563	9	HHTYR1	AF183604 Hylobates
24	272.6	90.9	1560	9	PATYR1	AF183634 Pygathrix
25	272.6	90.9	1560	9	PBTYR1	AF183684 Pygathrix
26	272.6	90.9	1563	9	TRFRTYR1	AF183674 Trachypit
27	272	90.7	1561	9	TPTYR1	AF183664 Trachypit
28	269.6	89.9	1561	9	HLTYP1	AF183609 Hylobates
29	267.8	89.3	1560	9	TLTYR1	AF183679 Trachypit
30	266	88.7	1554	9	NLTYP1	AF183639 Nasalis l
31	260.8	86.9	1560	6	POPTYR1	AF183644 Pongo pyg
32	235	78.3	3586	6	AX339194	AX339194 Sequence
33	229.6	76.5	1510	9	APTYR1	AF187155 Ateles pa
34	219	73.0	546	6	AX259950	AX259950 Sequence
35	219	73.0	546	6	AX262355	AX262355 Sequence
36	202.4	67.5	3586	6	AX339195	AX339195 Sequence
37	149.2	49.7	1169	9	GOGOTYR2	AF183599 Gorilla g
38	122	40.7	119000	9	AP001482	AP001482 Homo sapi
39	68.6	22.9	480	10	MMTYRGEN	X51743 Mouse tyros
40	68.6	22.9	4752	6	A37267	A37267 Sequence.7
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42	68.6	22.9	5505	2	AL831717	AI831717 Mus muscu
43	68.6	22.9	179598	2	AC084321	AC084321 Mus muscu
44	68.6	22.9	230967	2	AC122517	AC122517 Mus muscu
45	67.8	22.6	186161	2	AC106411	AC106411 Rattus no

ALIGNMENTS

RESULT 1
AX269131
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
human.
Sequence 2 from Patent WO0174861.
AX269131
AX269131.1 GI:16542051
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Vile, R.G., Harrington, K., Murphy, S. and Bateaman, A.
REFERENCES
AUTHORS
TITLE
Compositions and methods for tissue specific gene regulation
therapy

JOURNAL Patent: WO 0174861-A 2 11-OCT-2001;
MAYO FOUNDATION FOR MEDICAL EDUCATION AND RESEARCH (US)
FEATURES Location/Qualifiers
source 1..300
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 95 a 43 c 63 g 99 t
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Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 181 CGAAGAAAGTCAGTCATGCTTTTTCAGAGGATGAAGCTTAAGATAAAGACTAAAG 240
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Db 181 CGAAGAAAGTCAGTCATGCTTTTTCAGAGGATGAAGCTTAAGATAAAGACTAAAG 240
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Qy 241 TGTGTGATGCTGGAGTGGAGTGGTATTATATAGGCTCAGCCAAAGCATGTGATAATC 300
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Db 241 TGTGTGATGCTGGAGTGGAGTGGTATTATATAGGCTCAGCCAAAGCATGTGATAATC 300
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RESULT 2
HUMTYR01
LOCUS HUMTYR01 1629 bp DNA linear PRI 14-JAN-1995
DEFINITION Human tyrosinase gene, exon 1.
ACCESSION M63235 M60296
VERSION M63235.1 GI:340029
KEYWORDS tyrosinase.
SEGMENT 1 of 5
SOURCE Human DNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1629)
AUTHORS Giebel, L.B., Strunk, K.M. and Spritz, R.A.
TITLE Organization and nucleotide sequences of the human tyrosinase gene
and a truncated tyrosinase-related segment
JOURNAL Genomics 9 (3), 435-445 (1991)
MEDLINE 91236163
PUBMED 1903356
FEATURES Location/Qualifiers
source 1..1629
/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="llq14-q21"
590..1488
/note="minor 5' mRNA terminus"
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/evidence=experimental
exon 595..1488
/note="minor 5' mRNA terminus"
/number=1
/evidence=experimental
exon 624..1488
/note="major 5' mRNA terminus"
/number=1
/evidence=experimental
sig_peptide 670..723
/gene="TYR"
/note="G00-120-476"

BASE COUNT 469 a 342 c 353 g 465 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 7.6e-58;
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 351 AGGCATTATTATTACTAACCTTATTGTTAATATTCTACCATATAAGAAATTAACCTATTAA 410
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Qy 121 GGTGAATAGAGTTTTTCACTTTAATACATAGGCTATCCACATGTTGGGATACGAGCCAA 180
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Qy 181 CGAAGAAAGTCAGTCATGCTTTTTCAGAGGATGAAGCTTAAGATAAAGACTAAAG 240
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Db 471 CGAAGAAAGTCAGTCATGCTTTTTCAGAGGATGAAGCTTAAGATAAAGACTAAAG 530
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Qy 241 TGTGTGATGCTGGAGTGGAGTGGTATTATATAGGCTCAGCCAAAGCATGTGATAATC 300
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Db 531 TGTGTGATGCTGGAGTGGAGTGGTATTATATAGGCTCAGCCAAAGCATGTGATAATC 590
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RESULT 3
AR167367
LOCUS AR167367 2384 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 3 from patent US 6287569.
ACCESSION AR167367
VERSION AR167367.1 GI:17903142
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2384)
AUTHORS Kippes, T.J. and Wu, Y.
TITLE Vaccines with enhanced intracellular processing
JOURNAL Patent: US 6287569-A 3 11-SEP-2001;
FEATURES Location/Qualifiers
source 1..2384
/organism="unknown"
BASE COUNT 652 a 533 c 520 g 679 t
ORIGIN

Query Match 100.0%; Score 300; DB 6; Length 2384;
Best Local Similarity 100.0%; Pred. No. 7.1e-58;
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 AGGCATTATTATTACTAACCTTATTGTTAATATTCTACCATATAAGAAATTAACCTATTAA 120
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Qy 121 GGTGAATAGAGTTTTTCACTTTAATACATAGGCTATCCACATGTTGGGATACGAGCCAA 180
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Qy 181 CGAAGAAAGTCAGTCATGCTTTTTCAGAGGATGAAGCTTAAGATAAAGACTAAAG 240
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Db 304 CGAAGAAAGTCAGTCATGCTTTTTCAGAGGATGAAGCTTAAGATAAAGACTAAAG 363
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Qy 241 TGTGTGATGCTGGAGTGGAGTGGTATTATATAGGCTCAGCCAAAGCATGTGATAATC 300
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Db 364 TGTGTGATGCTGGAGTGGAGTGGTATTATATAGGCTCAGCCAAAGCATGTGATAATC 423
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RESULT 4

LOCUS E11466
DEFINITION CDNA encoding tyrosinase.
ACCESSION E11466
VERSION E11466.1 GI:22025102
KEYWORDS JP 1996140699-A/1.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2384)
Shibata,T., Suzuki,S., Takimoto,H. and Masui,S.
MEASUREMENT OF TYROSINASE MESSENGER RNA AMOUNT
Patent: JP 1996140699-A 1 04-JUN-1996;
POLA CHEM IND INC

COMMENT

OS Homo sapiens (human)
PN JP 1996140699-A/1
PD 04-JUN-1996
PF 22-NOV-1994 JP 1994288041
PI SHIBATA TAKASHI, SUZUKI SATOSHI, TAKIMOTO HIROYUKI, PI MASUI
SHIGEKI
PC C1201/68,C12N15/09;
CC strandedness: Double;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
FH Key
FH Location/Qualifiers
FT source
FT 1..2384
FT /organism="Homo sapiens"
FT /tissue_type="Skin"
FT /cell_type="melanocyte"
FT 5'UTR
FT CDS
FT 503..2092
FT /product="tyrosinase"
FT 2093..2384.
FT 3'UTR
FT Location/Qualifiers
FT 1..2384
FT /organism="Homo sapiens"
FT /db_xref="taxon:9606"

FEATURES

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BASE COUNT 652 a 533 c 520 g 679 t
ORIGIN

Query Match 100.0%; Score 300; DB 6; Length 2384;
Best Local Similarity 100.0%; Pred. No. 7.1e-58;
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 124 TCATTTCGAAGGTCAAATCATCATCTAGTTTGTAGTCTATTAACTGGGTTGCTTAGGTC 183
QY 61 AGGCATTATTATTACTAACTTATTTGTTAATATCTAACCATAGAATTAACCTATTAA 120
DB 184 AGGCATTATTATTACTAACTTATTTGTTAATATCTAACCATAGAATTAACCTATTAA 243
QY 121 GGTCAATAGAGTTTTTCACCTTTACATAGGCCTATCCCACTGGTGGGATACGAGCCAA 180
DB 244 GGTCAATAGAGTTTTTCACCTTTACATAGGCCTATCCCACTGGTGGGATACGAGCCAA 303
QY 181 CGAAGAAAAGTCAGTCATGCTGCTTTTCAGAGGATGAAGCTTAAGATAAGAGCTAAAG 240
DB 304 CGAAGAAAAGTCAGTCATGCTGCTTTTCAGAGGATGAAGCTTAAGATAAGAGCTAAAG 363
QY 241 TGTTTGATGCTGGAGGTGGGAGTGGTATTATATAGTCTCAGCCAAAGCTGTATATC 300
DB 364 TGTTTGATGCTGGAGGTGGGAGTGGTATTATATAGTCTCAGCCAAAGCTGTATATC 423

RESULT 5

LOCUS I49609
DEFINITION Sequence 1 from patent US 5641508.
PAT 07-OCT-1997

ACCESSION I49609
VERSION I49609.1 GI:2471829

KEYWORDS Unknown.

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 2384)

AUTHORS Li,L. and Lishko,V.K.

TITLE Method for delivering melanin to hair follicles

JOURNAL Patent: US 5641508-A 1 24-JUN-1997;

FEATURES Location/Qualifiers

source

1..2384

/organism="unknown"

BASE COUNT 652 a 533 c 520 g 679 t

ORIGIN

Query Match 100.0%; Score 300; DB 6; Length 2384;

Best Local Similarity 100.0%; Pred. No. 7.1e-58;

Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCATTTCGAAGGTCAAATCATCATCTAGTTTGTAGTCTATTAACTGGGTTGCTTAGGTC 60
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DB 304 CGAAGAAAAGTCAGTCATGCTGCTTTTCAGAGGATGAAGCTTAAGATAAGAGCTAAAG 363
QY 241 TGTTTGATGCTGGAGGTGGGAGTGGTATTATATAGTCTCAGCCAAAGCTGTATATC 300
DB 364 TGTTTGATGCTGGAGGTGGGAGTGGTATTATATAGTCTCAGCCAAAGCTGTATATC 423

RESULT 6

LOCUS HUMTYRA
DEFINITION Human tyrosinase (TYR) mRNA, complete cds.
ACCESSION M27160
VERSION M27160.1 GI:1698397

KEYWORDS tyrosinase.

SOURCE Homo sapiens.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 601 to 2384)

AUTHORS Shibahara,S., Tomita,Y., Tagami,H., Muller,R.M. and Cohen,T.

TITLE Molecular basis for the heterogeneity of human tyrosinase

JOURNAL Tohoku J. Exp. Med. 156 (4), 403-414 (1988)

MEDLINE 89222868

PUBMED 2854305

REFERENCE 2 (bases 1 to 600)

AUTHORS Takeda,A., Tomita,Y., Okinaga,S., Tagami,H. and Shibahara,S.

TITLE Functional analysis of the cDNA encoding human tyrosinase precursor

JOURNAL Biochem. Biophys. Res. Commun. 162 (3), 984-990 (1989)

MEDLINE 89351001

PUBMED 2504160

COMMENT On Dec 2, 1996 this sequence version replaced gi:340036.

Draft entry and computer-readable copy of sequence [1] kindly

provided by S.Shibahara, 15-AUG-1989.

FEATURES Location/Qualifiers

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520 g 679 t
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Query Match 100.0%; Score 300; DB 9; Length 2384;
Best Local Similarity 100.0%; Pred. No. 7.1e-58;
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCATTTCGAAGTCAATCATCATAGTTTGTAGTCTATTAACTGGGTTTCTTAGGTC 60
Db 124 TCATTTCGAAGTCAATCATCATAGTTTGTAGTCTATTAACTGGGTTTCTTAGGTC 183
QY 61 AGGCATTATTATTAACCTTATCTTAATCTTAACCATGAAGTAACTATTAAAT 120
Db 184 AGGCATTATTATTAACCTTATCTTAATCTTAACCATGAAGTAACTATTAAAT 243
QY 121 GGTGAATAGAGTTTTCACCTTAAACATAGGCTATCCCTACTGGTGATACGACCAATT 180
Db 244 GGTGAATAGAGTTTTCACCTTAAACATAGGCTATCCCTACTGGTGATACGACCAATT 303
QY 181 CGAAGAAAGTCAGTCATGTGCTTTTCAGAGATGAAGCTTTAAGATAAGACTAAAG 240
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QY 241 TGTTCATCTCGAGTGGGAGTGTATATATAGCTCTCACCAGACATCTGATAATC 300
Db 364 TGTTTGATGCTGGAGTGGAGTGGTATTATATAGGCTCTCAGCCAGACATCTGATAATC 423
RESULT 7
HSTYROIE HSTYROIE 3586 bp DNA linear PRI 20-NOV-1998
LOCUS Human tyrosinase gene, exon 1 and 5' flanking region (EC
DEFINITION 1.14.18.1).
ACCESSION X16073
VERSION X16073
KEYWORDS monophenol monooxygenase; tyrosinase.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3586)
```

```
Kikuchi, H.
Direct Submission
Submitted (03-AUG-1989) Kikuchi H., The Res. Inst. for TB and
Cancer, Tohoku University, 1-4 Seiryomachi, Sendai 980, JAPAN
REFERENCE 2 (bases 1 to 3586)
AUTHORS Kikuchi, H., Miura, H., Yamamoto, H., Takeuchi, T., Del. T. and
Watanabe, M.
TITLE Characteristic sequences in the upstream region of the human
tyrosinase gene
JOURNAL Biochim. Biophys. Acta 1009 (3), 283-286 (1989)
MEDLINE 90089403
PUBMED 2480811
COMMENT Data kindly reviewed (01-FEB-1990) by Kikuchi H.
FEATURES
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NGSTPMFNDINIYDLVNMHYVSDALLGSEIWRDIDFAHEAPAFPLPWHRLFLRW
EQEIOKLDGNDFTIPYWDWRDAEKDICTDEYMGQHTPNLPSASPSSSMOIVC
SRLEYNSHQSLCNGTPEGRLRNPNHDKRTPLPSSADVEFCLSLTOVESGMDK
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VDSIEOHLRHRPQLOEYVPEANAPIGHNRESYVFPFLYRNGDFFISSKDLGVDYS
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Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 668 AGGCATTATTATTACTAACCTTATTGTTAATATTCTAACCATAGAATTTAACTATTAAAT 727
Qy 121 GGTGAATAGAGTTTTCACATAGAGCCTATCCACCTGGTGGGATACGAGCCCAATT 180
Db 728 GGTGAATAGAGTTTTCACATAGAGCCTATCCACCTGGTGGGATACGAGCCCAATT 787
Qy 181 CGAAGAAAAGTCAGTCATGCTGCTTTTCAGAGGATGAAGCTTAAGATAAAGACTAAAG 240
Db 788 CGAAGAAAAGTCAGTCATGCTGCTTTTCAGAGGATGAAGCTTAAGATAAAGACTAAAG 847
Qy 241 TGTTCATGCTGGAGGTGGAGTGGTATTATATAGGTCCTCAGCCAAACACATGTCATATC 300
Db 848 TGTTCATGCTGGAGGTGGAGTGGTATTATATAGGTCCTCAGCCAAACACATGTCATATC 907

RESULT 8
LOCUS AP000720 147357 bp DNA linear PRI 23-MAY-2001
DEFINITION Homo sapiens genomic DNA, chromosome 11q clone:RP11-796A5, complete
sequences.
ACCESSION AP000720
VERSION AP000720.4 GI:14189775
KEYWORDS HFG.
SOURCE Homo sapiens DNA, clone:RP11-796A5.
ORGANISM Homo sapiens
REFERENCE 1 (sites)
AUTHORS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE Homo sapiens genomic DNA
JOURNAL Published Only in DataBase (1999)
REFERENCE 2 (bases 1 to 147357)
AUTHORS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE Direct Submission
JOURNAL Submitted (11-NOV-1999) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-cho,Tsukumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:hattori@gsc.riken.go.jp. URL:http://hgp.ygc.riken.go.jp/,
Tel:81-45-503-9111. Fax:81-45-503-9170)
COMMENT On May 22, 2001 this sequence version replaced gi:9927289.
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source
1. 147357
/organism="Homo sapiens"
/db_xref="taxon:9606"
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BASE COUNT 47827 a 26242 c 26214 g 47074 t
ORIGIN

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Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 AGGCATTATTATTACTAACCTTATTGTTAATATTCTAACCATAGAATTTAACTATTAAAT 120
Db 1776 AGGCATTATTATTACTAACCTTATTGTTAATATTCTAACCATAGAATTTAACTATTAAAT 1835
Qy 121 GGTGAATAGAGTTTTCACATAGAGCCTATCCACCTGGTGGGATACGAGCCCAATT 180
Db 1836 GGTGAATAGAGTTTTCACATAGAGCCTATCCACCTGGTGGGATACGAGCCCAATT 1895
Qy 181 CGAAGAAAAGTCAGTCATGCTGCTTTTCAGAGGATGAAGCTTAAGATAAAGACTAAAG 240
Db 1896 CGAAGAAAAGTCAGTCATGCTGCTTTTCAGAGGATGAAGCTTAAGATAAAGACTAAAG 1955
Qy 241 TGTTCATGCTGGAGGTGGAGTGGTATTATATAGGTCCTCAGCCAAACACATGTCATATC 300

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Db 1956 TGTTCATGCTGGAGGTGGAGTGGTATTATATAGGTCCTCAGCCAAAGCATGTCATAATC 2015

RESULT 9
LOCUS PAPATYR1 1563 bp DNA linear PRI 29-OCT-2000
DEFINITION Pan paniscus tyrosinase gene, exon 1.
ACCESSION AF183588
VERSION AF183588.1 GI:11036743
KEYWORDS 1 of 5
SEGMENT SOURCE
ORGANISM Pan paniscus.
Pan paniscus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE 1 (bases 1 to 1563)
AUTHORS Ding,B., Ryder,O.A., Shi,P. and Zhang,Y.-P.
TITLE Molecular evolution of tyrosinase gene in primates
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1563)
AUTHORS Ding,B., Ryder,O.A., Shi,P. and Zhang,Y.-P.
TITLE Direct Submission
JOURNAL Submitted (09-SEP-1999) Laboratory of Cellular and Molecular
Evolution, Kunming Institute of Zoology, the Chinese Academy of
Sciences, 32 Jiao Chang Dong Lu, Kunming, Yunnan 550223, P.R. China
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1. 1563
/organism="Pan paniscus"
/db_xref="taxon:9597"
<628.1446
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BASE COUNT 449 a 332 c 336 g 446 t
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Best Local Similarity 98.7%; Pred. No. 2.1e-56;
Matches 296; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy 61 AGGCATTATTATTACTAACCTTATTGTTAATATTCTAACCATAGAATTTAACTATTAAAT 120
Db 309 AGGCATTATTATTACTAATCTTATTGTTAATATTCTAACCATAGAATTTAACTATTAAAT 368
Qy 121 GGTGAATAGAGTTTTCACATAGAGCCTATCCACCTGGTGGGATACGAGCCCAATT 180
Db 369 GGTGAATAGAGTTTTCACATAGAGCCTATCCACCTGGTGGGATACGAGCCCAATT 428
Qy 181 CGAAGAAAAGTCAGTCATGCTGCTTTTCAGAGGATGAAGCTTAAGATAAAGACTAAAG 240
Db 429 CGAAGAAAAGTCAGTCATGCTGCTTTTCAGAGGATGAAGCTTAAGATAAAGACTAAAG 488
Qy 241 TGTTCATGCTGGAGGTGGAGTGGTATTATATAGGTCCTCAGCCAAACACATGTCATATC 300
Db 489 TGTTCATGCTGGAGGTGGAGTGGTATTATATAGGTCCTCAGCCAAACACATGTCATATC 548

RESULT 10
LOCUS PTTYR1 1563 bp DNA linear PRI 26-OCT-2000
DEFINITION Pan troglodytes tyrosinase gene, exon 1.
ACCESSION AF183588
VERSION AF183588.1 GI:11023097
KEYWORDS 1 of 5
SEGMENT SOURCE
ORGANISM Pan troglodytes.
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE 1 (bases 1 to 1563)

```

AUTHORS Ding, B., Ryder, O.A., Shi, P. and Zhang, Y.-P.
TITLE Molecular evolution of tyrosinase gene in primates
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1563)
AUTHORS Ding, B., Ryder, O.A., Shi, P. and Zhang, Y.-P.
TITLE Direct Submission
JOURNAL Submitted (09-SEP-1999) Laboratory of Cellular and Molecular Evolution, Kunming Institute of Zoology, the Chinese Academy of Sciences, 32 Jiao Chang Dong Lu, Kunming, Yunnan 650223, P.R. China

FEATURES
source Location/Qualifiers
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/number=1
BASE COUNT 446 a 334 c 336 g 447 t
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Matches 295; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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QY 121 GGTGAATAGAGTTTTCACCTTAAACATAGGCTATCCCACTGGTGGATACGACCAAT 180
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QY 181 CGAAGAAAAGTCAGTCATGCTTTTCAGAGGATGAAAGCTTAAGATAAGACTAAAAG 240
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DB 429 CGAAGAAAAGTCAGTCATGCTTTTCAGAGGATGAAAGCTTAAGATAAGACTAAAAG 488
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QY 241 TGTTCATGCTGGAGTGGAGTGGTATTATATAGTCTCAGCCCAAGACATGTGATAATC 300
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DB 489 TGTTCATGCTGGAGTGGAGTGGTATTATATAGTCTCAGCCCAAGACATGTGATAATC 548
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RESULT 11
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LOCUS HSU03039 2311 bp DNA linear PRI 06-AUG-1994
DEFINITION Human tyrosinase gene, promoter region.
ACCESSION U03039
VERSION U03039.1 GI:414980
KEYWORDS human.
SOURCE Homo sapiens

ORGANISM
Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 2311)
Ponnazhagan, S., Hou, L. and Kwon, B.S.
STRUCTURAL organization of the human tyrosinase gene and sequence analysis and characterization of its promoter region
J. Invest. Dermatol. 102 (5), 744-748 (1994)
94231032
PUBMED 8176257
REFERENCE 2 (bases 1 to 2311)
Kwon, B.S.
Direct Submission
Submitted (29-OCT-1993) Kwon B.S., Indiana University School of Medicine, Microbiology and Immunology, 635 Barnhill Dr., Indianapolis, IN 46202, USA
Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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/cell_type="melanocyte"

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/gene="tyrosinase gene"
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BASE COUNT 796 a 396 c 493 g 626 t
ORIGIN

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Matches 300; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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QY 61 AGCCATTATTACTAACTTATGTTTAAATTTCTAACCAATAAGAAATTAACATAAT 120
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DB 1989 AGCCATTATTACTAACTTATGTTTAAATTTCTAACCAATAAGAAATTAACATAAT 2048
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QY 121 GGTGAATAGAGTTTTCACCTTAAACATAGGCTATCCCACTGGTGGATACGACCAAT 180
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DB 2049 GGTGAATAGAGTTTTCACCTTAAACATAGGCTATCCCACTGGTGGATACGACCAAT 2108
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QY 181 CGAAG-AAAAGTCAGTCATGCTTTTCAGAGGATGAAAGCTTAAGATAAGACTAAA 239
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DB 2109 CGAAGAAAAGTCAGTCATGCTTTTCAGAGGATGAAAGCTTAAGATAAGACTAAA 2168
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QY 240 GTGTTTGATGCTGGAGTGGAGTGGTATTATATAGTCTCAGCCCAAGACATGTGATAAT 299
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DB 2169 GTGTTTGATGCTGGAGTGGAGTGGTATTATATAGTCTCAGCCCAAGACATGTGATAAT 2228
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QY 300 c 300
DB 2229 c 2229

RESULT 12
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LOCUS I70158 2397 bp DNA linear PAT 02-APR-1998
DEFINITION Sequence 11 from patent US 5679511.
ACCESSION I70158
VERSION I70158.1 GI:3006293
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2397)
AUTHORS Kwon, B.S.
TITLE CDNA clones for a regulatory protein in the melanin-production pathway
JOURNAL Patent: US 5679511-A 11 21-OCT-1997;
FEATURES Location/Qualifiers
source 1..2397
/organism="unknown"
BASE COUNT 808 a 427 c 507 g 655 t
ORIGIN

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Best Local Similarity 99.7%; Pred. No. 2.1e-55;
Matches 300; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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DB 1926 TCATTTCGAAGTCAAAATCATCATAGTTTGTAGTCTATTAACTGGGTTTCTTAGGTC 1985
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QY 61 AGCCATTATTACTAACTTATGTTTAAATTTCTAACCAATAAGAAATTAACATAAT 120
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DB 1986 AGCCATTATTACTAACTTATGTTTAAATTTCTAACCAATAAGAAATTAACATAAT 2045
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QY 121 GGTGAATAGAGTTTTCACCTTAAACATAGGCTATCCCACTGGTGGATACGACCAAT 180
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DB 2046 GGTGAATAGAGTTTTCACCTTAAACATAGGCTATCCCACTGGTGGATACGACCAAT 2105
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Qy	300	C 300	
Dd	2226	C 2226	
RESULT 13			
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LOCUS	MNTYR1	1557 bp DNA linear	PRI 26-OCT-2000
DEFINITION	Macaca nemestrina tyrosinase gene, exon 1.		
ACCESSION	AF183578		
VERSION .	AF183578.1 GI:11023089		
KEYWORDS	1 of 5		
SEGMENT	Macaca nemestrina.		
SOURCE	Macaca nemestrina.		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Cercopithecinae; Macaca. 1 (bases 1 to 1557) Ding,B., Ryder,O.A., Shi,P. and Zhang,Y.-P. Molecular evolution of tyrosinase gene in primates Unpublished 2 (bases 1 to 1557) Ding,B., Ryder,O.A., Shi,P. and Zhang,Y.-P. Direct Submission Submitted (09-SEP-1999) Laboratory of Cellular and Molecular Evolution, Kunming Institute of Zoology, the Chinese Academy of Sciences, 32 Jiao Chang Dong Lu, Kunming, Yunnan 650223, P.R. China		
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
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Best Local Similarity	97.3%;	Pred. No. 5.8e-55;	
Matches 292;	Conservative 0;	Mismatches 8;	Indels 0; Gaps 0;
Qy	1	TCATTTCAAGGTCACCATCATCATAGTTTGTAGTCTATTAAGTGGGTTTGCCTTAGGTC	60
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Qy	61	AGGCATTATTATTACTAACCTTATGTTTAATTTCTTAACCATAGAATTAACAATTATAAT	120
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Dd	423	CCAAGAAGTCAAGTCAGTCATGCTGCTTTTCACAGGATGAAAGCTTAAGATAAAGACTAAAA	482
Qy	241	TGTTTGATGCTGGAGTGGGAGTGGTATTATAGGCTCTCAGCCAAGACATGTGATAATC	300
Dd	483	TGTTTGATGCTGGAGTGGGAGTGGTATTATAGGCTCTCAGCCAAGACATGTGATAATC	542
RESULT 14			
COPYTYR1			

LOCUS	COPOYR1	1558 bp	DNA	linear	PRI 29-OCT-2000
DEFINITION	Colobus polykomos tyrosinase gene, exon 1.				
ACCESSION	AF183593				
VERSION	AF183593.1	GI:11036702			
KEYWORDS					
SEGMENT	1 of 5				
SOURCE	Colobus polykomos.				
ORGANISM	Colobus polykomos				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae; Colobinae; Colobus.				
REFERENCE	1 (bases 1 to 1558)				
AUTHORS	Ding, B., Ryder, O.A., Shi, P. and Zhang, Y.-P.				
TITLE	Molecular evolution of tyrosinase gene in primates				
JOURNAL	Unpublished				
REFERENCE	2 (bases 1 to 1558)				
AUTHORS	Ding, B., Ryder, O.A., Shi, P. and Zhang, Y.-P.				
TITLE	Direct Submission				
JOURNAL	Submitted (09-SEP-1999) Laboratory of Cellular and Molecular Evolution, Kunming Institute of Zoology, The Chinese Academy of Sciences, 32 Jiao Chang Dong Lu, Kunming, Yunnan 650223, P.R.China				
FEATURES	Location/Qualifiers				
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Db	303 AGGCATTATTATTATTATCTTATTGTTAATTTCTTAACCATAGAAATTAACATAATTAAT 362				
Qy	121 GGTCAATAGAGTTTTTTCACTTTACATAGGCTATCCACATGGTGGGATAGAGCAAAAT 180				
Db	363 GGTCAATAGAGTTTTTTCACTTTACATAGAGCTATCCACATGGTGGGATAGAGCAAAAT 422				
Qy	181 CGAAGAAAAGTCAGTCATGTGCTTTTCAGAGGATGAAAGCTTAAGATAAGACTATAAAG 240				
Db	423 CCAAGAAAAGTCAGTCATGTGCTTTTCAGAGGATGAAAGCTTAAGATAAGACTATAAAG 482				
Qy	241 TGTTTGATGCTGGAGGTGGAGTGGTATTATATAGGTCACGCCAAGACATGTGATAATC 300				
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RESULT 15					
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LOCUS	MATYR1	1558 bp	DNA	linear	PRI 01-NOV-2000
DEFINITION	Macaca arctoides tyrosinase gene, exon 1.				
ACCESSION	AF183614				
VERSION	AF183614.1	GI:1105814			
KEYWORDS					
SEGMENT	1 of 5				
SOURCE	Macaca arctoides.				
ORGANISM	Macaca arctoides				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae; Cercopitheciinae; Macaca.				
REFERENCE	1 (bases 1 to 1558)				
AUTHORS	Ding, B., Ryder, O.A., Shi, P. and Zhang, Y.-P.				
TITLE	Molecular evolution of tyrosinase gene in primates				
JOURNAL	Unpublished				
REFERENCE	2 (bases 1 to 1558)				

AUTHORS Ding, B., Ryder, O.A., Shi, P. and Zhang, Y.-P.
TITLE Direct Submission
JOURNAL Submitted (09-SEP-1999) Laboratory of Cellular and Molecular
Evolution, Kunming Institute of Zoology, The Chinese Academy of
Sciences, 32 Jiao Chang Dong Lu, Kunming, Yunnan 650223, P.R. China
FEATURES Location/Qualifiers
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BASE COUNT 445 a 329 c 343 g 441 t
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Best Local Similarity 97.3%; Pred. No. 5.8e-55;
Matches 292; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 1 TCATTTGCAAGTCAAAATCATCATAGTTTGTAGTCTATTAACTGGGTTTGGTTAGGTC 60
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QY 181 CGAAGAAAAGTCAGTCATGTGCTTTTCAGAGGATGAAGCTTAAGATAAGACTAAAAG 240
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Db 483 TGTTCATGCTGGAGTGGAGTGGTATTATATAGTCTCAGCCAAAGACATGTGATAATC 542

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OM nucleic - nucleic search, using sw model

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SUMMARIES

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2	300	100.0	300	23 AAS14779	Melanoma-specific
3	300	100.0	2384	15 AAQ72871	Human tyrosinase g
4	300	100.0	2384	17 AAT33316	Tyrosinase mRNA.
5	300	100.0	3586	15 AAQ56643	Human tyrosinase g
6	289	96.3	2397	18 AAT95736	Human tyrosinase g
7	235	78.3	3586	24 AAS63366	Chemically pretrea
8	219	73.0	546	22 AAH43616	Tyrosinase-TRE. H
9	219	73.0	546	23 AAF87236	Tyrosinase-TRE fus

c	10	202.4	67.5	3586	24	AAS63367	Chemically pretrea
c	11	67	22.3	4752	15	AAQ58032	Tyrosinase promote
c	12	42.4	14.1	1212	21	AAA70218	Plasmodium falcipa
c	13	40.8	13.6	7195	22	AAS45324	Chemically pretrea
c	14	40.8	13.6	7195	24	ABK28165	DNA transcription
c	15	40	13.3	2041	22	AAS60958	Human cancer agent
c	16	38.8	12.9	3582	21	AAA70241	Plasmodium falcipa
c	17	38.2	12.7	9021	22	AAS46326	Tyrosinase suppressor
c	18	37.8	12.6	15767	24	ABL33207	Human immune syste
c	19	37.8	12.6	15767	24	ABL34553	Human metastasis a
c	20	37.6	12.5	382	21	ABN81050	Shrimp polynucleot
c	21	37.2	12.4	2270	23	ABL24848	Drosophila melanog
c	22	37.2	12.4	1143	23	ABL12834	Drosophila melanog
c	23	37	12.3	5454	21	AAA70236	Plasmodium falcipa
c	24	36.6	12.2	357	21	AAZ94801	Soybean microsate
c	25	36.6	12.2	580	21	ABN81132	Shrimp polynucleot
c	26	36.6	12.2	2924	22	AAH55011	S. epidermidis gen
c	27	36.6	12.2	3037	22	AAH54537	S. epidermidis gen
c	28	36.6	12.2	3241	22	AAH54912	S. epidermidis gen
c	29	36.4	12.1	944	23	ABL13085	Drosophila melanog
c	30	36.4	12.1	1835	23	ABL20020	Drosophila melanog
c	31	36.4	12.1	1835	23	ABL20898	Drosophila melanog
c	32	36.4	12.1	2948	23	ABL13084	Drosophila melanog
c	33	36.4	12.1	6642	23	ABL05270	Drosophila melanog
c	34	36.4	12.1	10810	23	ABL13100	Drosophila melanog
c	35	36.4	12.1	10992	23	ABL05242	Drosophila melanog
c	36	36.4	12.1	15649	22	AAS45396	Chemically pretrea
c	37	36.4	12.1	15649	24	ABK28241	LNA transcription
c	38	36.2	12.1	925	21	ABN81142	Shrimp polynucleot
c	39	36.2	12.1	6033	21	AAA70152	Plasmodium falcipa
c	40	36.2	12.1	8654	23	ABL04334	Drosophila melanog
c	41	36.2	12.1	12943	23	ABL20980	Drosophila melanog
c	42	36	12.0	373	21	ABN81130	Shrimp polynucleot
c	43	36	12.0	1452	21	AAA70123	Plasmodium falcipa
c	44	36	12.0	19576	24	ABL70576	Chemically treated
c	45	36	12.0	19576	24	AAS61259	Human gene regulat

ALIGNMENTS

RESULT 1

AAC86171
ID AAC86171 standard; cDNA; 300 BP.

XX AAC86171;

XX 19-SEP-2001 (first entry)

XX Tyr300.

XX DE

XX KW

XX KW

XX KW

XX OS

XX FH

XX FT

XX FT

XX PN

XX PD

XX PF

XX PR

XX PA

XX PI

XX XX

Melanoma-specific promoter; human; tyrosinase gene; Tyr300; M box;
activator; transgene expression; gene therapy; tumour; melanoma; ss.

Homo sapiens.

Key Location/Qualifiers
misc_signal 194..204
/*tag= a
/label= "M box"

WO200138488-A2.

31-MAY-2001.

22-NOV-2000; 2000WO-US32203.

23-NOV-1999; 99US-0167085.

(MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.

Vile R, Gough M;

DR WPI: 2001-367671/38.
XX Novel nucleic acid construct for cell type-specific expression of
PT therapeutic transgene, comprising a cell type-specific promoter
PT operably linked to therapeutic gene, and amplification promoter element
PT
XX
XX
PS Claim 9; Page 16; 33pp; English.
XX This sequence represents the minimal melanoma-specific promoter
CC corresponding to bases -300 to -1 of the human tyrosinase gene
CC (Tyr300). Tyr300 is a subsequence of the 5' untranslated region of
CC the human tyrosinase gene and contains at least four positive DNA
CC binding elements as one as one negative element. The M box, found at
CC -107 to -97 is a conserved element found in other melanocyte-specific
CC promoters. When Tyr300 is incorporated into a recombinant construct,
CC it functions as a highly selective activator for transgene expression
CC in melanoma cells. Constructs such as these are useful for gene
CC therapy of tumours such as melanoma, cancers, genetic diseases and other
CC ailments amenable to gene therapy.
XX
SQ Sequence 300 BP; 95 A; 43 C; 63 G; 99 T; 0 other;
Query Match 100.0%; Score 300; DB 22; Length 300;
Best Local Similarity 100.0%; Pred. No. 3.2e-68;
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCATTGCAAGGTCAATCATCATTTGTTAGTCTATTAACTGGGTTTGGCTTAGGTC 60
DB 1 TCATTGCAAGGTCAATCATCATTTGTTAGTCTATTAACTGGGTTTGGCTTAGGTC 60
QY 61 AGGCATTATTATTACTACCTTATGTTAATATTCTTACCATAGAAATTAACATTAAAT 120
DB 61 AGGCATTATTATTACTACCTTATGTTAATATTCTTACCATAGAAATTAACATTAAAT 120
QY 121 GGTGAATAGAGTTTTCACCTTAACTAGGCTATCCACCTGGTGGGATACGACCAATT 180
DB 121 GGTGAATAGAGTTTTCACCTTAACTAGGCTATCCACCTGGTGGGATACGACCAATT 180
QY 181 CGAAGAAAAGTCATGCTGCTTTTCAGAGGATGAAAGCTTAAGATAAAGACTAAAG 240
DB 181 CGAAGAAAAGTCATGCTGCTTTTCAGAGGATGAAAGCTTAAGATAAAGACTAAAG 240
QY 241 TGTGTTGATGCTGGAGTGGGAGTGCTATTATATAGTCTCAGCCAGACATGTGATAATC 300
DB 241 TGTGTTGATGCTGGAGTGGGAGTGCTATTATATAGTCTCAGCCAGACATGTGATAATC 300
RESULT 2
AAS14779
ID AAS14779 standard; DNA; 300 BP.
XX
AC AAS14779;
XX
XX
DT 27-FEB-2002 (first entry)
XX
DE Melanoma-specific human tyrosinase promoter sequence.
XX
KW Recombinant nucleic acid vector; carcinoembryonic antigen; CEA; cytokine;
KW syncytium-inducing polypeptide; fusogenic membrane glycoprotein; tumour;
KW recombinase; tumour-specific promoter; hypoxic response element; HRE; ds;
KW tyrosinase promoter; Cre; FLP; retroviral vector; malignant cell; cancer;
KW cytostatic; gene therapy; human; melanoma.
XX
OS Homo sapiens.
XX
PN WO200174861-A2.
XX
PD 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US10250.
XX
XX 31-MAR-2000; 2000US-193977P.

XX (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
XX Ville RG, Harrington K, Murphy S, Bateman A;
XX WPI: 2001-656985/75.
XX Recombinant nucleic acid vector for reducing tumour size, has expression
PT cassette comprising a promoter linked to nucleic acid sequence encoding
PT a syncytium-inducing polypeptide and flanked on either side by
PT recombinase
XX
XX Disclosure; Fig 4; 84pp; English.
XX The invention relates to a recombinant nucleic acid vector comprising a
CC first expression cassette, comprising a first promoter operably linked to
CC a nucleic acid sequence encoding a syncytium-inducing polypeptide (such
CC as a fusogenic membrane glycoprotein) and flanked on either side by a
CC sequence recognised by a recombinase, and/or a second expression cassette
CC comprising a tumour-specific promoter operably linked to a nucleic acid
CC sequence encoding a recombinase. The nucleic acid of the first expression
CC cassette may be linked to a hypoxic response element (HRE), the second
CC expression cassette may contain a promoter linked to a nucleic acid
CC promoter linked to the nucleic acid encoding the recombinase. The tumour
CC specific promoter is, for example, a carcinoembryonic antigen (CEA)
CC promoter or a tyrosinase promoter, and the recombinase is, for example,
CC Cre recombinase or FLP recombinase. The invention is useful for reducing
CC tumour size by administering the compositions as retroviral vectors, or
CC in a cell containing the vector, to an individual in need of treatment
CC for a disease caused by malignant cells. This sequence represents a
CC melanoma-specific human tyrosinase promoter.
XX
SQ Sequence 300 BP; 95 A; 43 C; 63 G; 99 T; 0 other;
Query Match 100.0%; Score 300; DB 23; Length 300;
Best Local Similarity 100.0%; Pred. No. 3.2e-68;
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCATTGCAAGGTCAATCATCATTTGTTAGTCTATTAACTGGGTTTGGCTTAGGTC 60
DB 1 TCATTGCAAGGTCAATCATCATTTGTTAGTCTATTAACTGGGTTTGGCTTAGGTC 60
QY 61 AGGCATTATTATTACTACCTTATGTTAATATTCTTACCATAGAAATTAACATTAAAT 120
DB 61 AGGCATTATTATTACTACCTTATGTTAATATTCTTACCATAGAAATTAACATTAAAT 120
QY 121 GGTGAATAGAGTTTTCACCTTAACTAGGCTATCCACCTGGTGGGATACGACCAATT 180
DB 121 GGTGAATAGAGTTTTCACCTTAACTAGGCTATCCACCTGGTGGGATACGACCAATT 180
QY 181 CGAAGAAAAGTCATGCTGCTTTTCAGAGGATGAAAGCTTAAGATAAAGACTAAAG 240
DB 181 CGAAGAAAAGTCATGCTGCTTTTCAGAGGATGAAAGCTTAAGATAAAGACTAAAG 240
QY 241 TGTGTTGATGCTGGAGTGGGAGTGCTATTATATAGTCTCAGCCAGACATGTGATAATC 300
DB 241 TGTGTTGATGCTGGAGTGGGAGTGCTATTATATAGTCTCAGCCAGACATGTGATAATC 300
RESULT 3
AAQ72871
ID AAQ72871 standard; cDNA; 2384 BP.
XX
AC AAQ72871;
XX
XX 21-JUN-1995 (first entry)
XX Human tyrosinase gene.
XX
XX Human; tyrosinase; compound; hair; follicle; liposome; lipophilic;
KW lipophobic; stratum corneum; melanin; hair dye; glycoprotein; alopecia;
KW chemotherapy; transforming growth factor; growth stimulant; aromatase;
KW

```

KW cyclosporin A; macromolecule; polymer; ss.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 503..2092
XX FT /*tag= a
XX FT /product= human tyrosinase
XX
XX WO9422468-A.
XX
XX 13-OCT-1994.
XX
XX 01-APR-1994; 94WO-US03634.
XX
XX 02-APR-1993; 93US-0041553.
XX 13-JAN-1994; 94US-0181471.
XX
XX (ANTI-) ANTICANCER INC.
XX
XX Li L, Lishko VK;
XX
XX WPI; 1994-332816/41.
XX P-PSDB; AAR63623.
XX
XX Liposomes for delivering protein, nucleic acid etc. to hair
XX follicles - e.g. to restore hair colour, prevent hair loss during
XX chemotherapy, stimulate hair growth etc.
XX
XX Claim 6; Page 67-70; 10pp; English.
XX
XX The nucleotide sequence of a human tyrosinase gene. This is an example
XX of a compound which can be delivered to hair follicles via a novel
XX liposome composition. The liposomes are comprised of a lipophilic or
XX lipophobic compound which will selectively target the hair follicle
XX (via the stratum corneum) without damaging or unwanted effects on cells
XX outside the follicle. Compounds e.g. tyrosinase (or the DNA encoding
XX it), melanin or hair dyes, can be delivered to the hair follicle to
XX restore hair colour or condition. Other compounds targeted at hair
XX follicles can include; p-glycoprotein (AAQ72872) (for treatment of
XX chemotherapy-induced alopecia); human transforming growth factor alpha
XX (AAQ2873) (for reversal of wavy hair); hair growth stimulants (e.g.
XX cyclosporin A or aramase) or antisense sequences. The methods allows
XX compounds (e.g. macromolecules or polymers), which would not normally
XX reach the hair follicles, to be delivered to these target areas.
XX
XX Sequence 2384 BP; 652 A; 534 C; 519 G; 679 T; 0 other;
XX
XX
XX Query Match 100.0%; Score 300; DB 15; Length 2384;
XX Best Local Similarity 100.0%; Pred. No. 4.9e-68;
XX Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 TCATTTGCAAGGTCATCATCATCTAGTTTGTAGTCTATTAACTGGTTGCTTAGGTC 60
XX |||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 124 TCATTTGCAAGGTCATCATCATCTAGTTTGTAGTCTATTAACTGGTTGCTTAGGTC 183
XX |||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX
XX 61 AGGCATTATTATTACTAACCTTATTGTTATATTCTAACCATAGAACTAACTATTAAT 120
XX |||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX
XX 184 AGGCATTATTATTACTAACCTTATTGTTATATTCTAACCATAGAACTAACTATTAAT 243
XX |||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX
XX 121 GGTGAATAGAGTTTTCACCTTTAACATPAGCCCTATCCCACTGGTGGGATACGAGCAATT 180
XX |||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX
XX 244 GGTGAATAGAGTTTTCACCTTTAACATPAGCCCTATCCCACTGGTGGGATACGAGCAATT 303
XX |||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX
XX 181 CGAAGAAAGTCAGTCATGCTGCTTTTCAGAGCATGAACTTAACATAAGACTAAAG 240
XX |||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX
XX 304 CGAAGAAAGTCAGTCATGCTGCTTTTCAGAGCATGAACTTAACATAAGACTAAAG 363
XX |||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX
XX 241 TGTTTGTATGCTGGAGGTGGAGTGGTATTATATAGGTCTCAGCCAGACATGTGATAATC 300
XX |||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX
XX 364 TGTTTGTATGCTGGAGGTGGAGTGGTATTATATAGGTCTCAGCCAGACATGTGATAATC 423
XX |||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX
XX
XX RESULT 4
XX AAT33316
XX ID AAT33316 standard; CDNA to mRNA; 2384 BP.
XX
XX AC AAT33316;
XX
XX DT 18-OCT-1996 (first entry)
XX
XX DE Tyrosinase mRNA.
XX
XX KW Human; tyrosinase; detection; primer; reverse transcription; amplify;
XX KW transcription region; detection; ds.
XX
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
XX CDS 503..2092
XX FT /*tag= a
XX FT /product= Tyrosinase
XX FT 790..810
XX FT /*tag= b
XX FT /note= "Binds primer given in AAT33323"
XX FT 881..901
XX FT /*tag= c
XX FT /note= "Binds primer given in AAT33321"
XX FT 1297..1317
XX FT /*tag= d
XX FT /note= "Binds primer given in AAT33317"
XX FT 1327..1347
XX FT /*tag= e
XX FT /note= "Binds primer given in AAT33319"
XX FT complement (1521..1541)
XX FT /*tag= f
XX FT /note= "Binds primer given in AAT33318"
XX FT complement (1600..1620)
XX FT /*tag= g
XX FT /note= "Binds primer given in AAT33332"
XX FT complement (1650..1670)
XX FT /*tag= h
XX FT /note= "Binds primer given in AAT33320"
XX FT complement (1673..1693)
XX FT /*tag= i
XX FT /note= "Binds primer given in AAT33324"
XX
XX JP08140699-A.
XX
XX 04-JUN-1996.
XX
XX 22-NOV-1994; 94JP-0288041.
XX
XX 22-NOV-1994; 94JP-0288041.
XX (POKK ) POLA CHEM IND INC.
XX
XX WPI; 1996-316329/32.
XX P-PSDB; AAW00184.
XX
XX Detection of tyrosinase mRNA - by amplification of tyrosinase mRNA
XX allows accurate detection of trace amounts of RNA
XX
XX Disclosure; Page 7-9; 10pp; Japanese.
XX
XX This sequence encodes human tyrosinase. This sequence was detected
XX by the method of the invention using the primers given in AAT33317-24.
XX The method comprises synthesising tyrosinase cDNA from a sample by
XX reverse transcription and then amplifying the cDNA using primers
XX specific for, or complementary to, sequences within the transcription
XX region of the tyrosinase gene. Amplification using these primers
XX produces a competitive cDNA which can also be amplified. This method
XX can be used to specifically detect trace amounts of human tyrosinase
XX mRNA.
XX
XX Sequence 2384 BP; 652 A; 533 C; 520 G; 679 T; 0 other;
XX
```

```
Query Match      100.0%; Score 300; DB 17; Length 2384;
Best Local Similarity 100.0%; Pred. No. 4.9e-69;
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCATTGCAAGTCAAAATCATCATTTGTTAGTCTATTAACTGGGTTGCTTAGGTC 60
DB 124 TCATTGCAAGTCAAAATCATCATTTGTTAGTCTATTAACTGGGTTGCTTAGGTC 183

QY 61 AGGCATTATTACTAACCTTATTGTTAAATTTCTAACCATTAAGAAATAACTATTAA 120
DB 184 AGGCATTATTACTAACCTTATTGTTAAATTTCTAACCATTAAGAAATAACTATTAA 243

QY 121 GGTGAATAGAGTTTTCACCTTTAACATAGGCTATCCACCTGGTGGGATACGACCAATT 180
DB 244 GGTGAATAGAGTTTTCACCTTTAACATAGGCTATCCACCTGGTGGGATACGACCAATT 303

QY 181 CGAAGAAAAGTCAGTCATGTCTTTTCAGAGGATGAAGCTTAAAGATAAGACTAAAAG 240
DB 304 CGAAGAAAAGTCAGTCATGTCTTTTCAGAGGATGAAGCTTAAAGATAAGACTAAAAG 363

QY 241 TGTTCATGCTGGAGTGGAGTGGTATTATATAGGTCTCAGCCCAAGACATGTGATAATC 300
DB 364 TGTTCATGCTGGAGTGGAGTGGTATTATATAGGTCTCAGCCCAAGACATGTGATAATC 423

RESULT 5
AAQ56643
ID AAQ56643 standard; DNA; 3586 BP.
XX AC AAQ56643;
XX DT 16-SEP-1994 (first entry)
XX DE Human tyrosinase gene.
XX KW Tyrosinase; albino; albinism; detection; diagnosis;
XX KW treatment; prevention; ss.
XX OS Homo sapiens.
XX FH Key
XX FT CDS
XX FT Location/Qualifiers
XX FT 987..1805
XX FT /*tag= a
XX FT /product= Tyrosinase.
XX FT /note= "CDS excludes termination codon."
XX PN JP06000100-A.
XX PD 11-JAN-1994.
XX PF 18-JUN-1992; 92JP-0185885.
XX PR 18-JUN-1992; 92JP-0185885.
XX PA (DAI) DAICEL CHEM IND LTD.
XX DR WPI; 1994-077141/10.
XX DR P-PSDB; AAR48368.
XX PT A DNA sequence which hybridises to the human tyrosinase gene -
XX PT used for the detection, diagnosis, prevention and treatment of
XX PT human albinism
XX PS Disclosure; Page 5-7; 8pp; Japanese.
XX CC A DNA sequence having at least 12 successive bases and which
XX CC hybridises upstream and/or downstream of the 310th base from the
XX CC transcription start site of the human tyrosinase gene can be
XX CC used for the detection, diagnosis, prevention and treatment of human
XX CC albinism.
XX SQ Sequence 3586 BP; 1127 A; 636 C; 760 G; 1063 T; 0 other;
```

```
Query Match      100.0%; Score 300; DB 15; Length 3586;
Best Local Similarity 100.0%; Pred. No. 5.3e-68;
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCATTGCAAGTCAAAATCATCATTTGTTAGTCTATTAACTGGGTTGCTTAGGTC 60
DB 608 TCATTGCAAGTCAAAATCATCATTTGTTAGTCTATTAACTGGGTTGCTTAGGTC 667

QY 61 AGGCATTATTACTAACCTTATTGTTAAATTTCTAACCATTAAGAAATAACTATTAA 120
DB 668 AGGCATTATTACTAACCTTATTGTTAAATTTCTAACCATTAAGAAATAACTATTAA 727

QY 121 GGTGAATAGAGTTTTCACCTTTAACATAGGCTATCCACCTGGTGGGATACGACCAATT 180
DB 728 GGTGAATAGAGTTTTCACCTTTAACATAGGCTATCCACCTGGTGGGATACGACCAATT 787

QY 181 CGAAGAAAAGTCAGTCATGTCTTTTCAGAGGATGAAGCTTAAAGATAAGACTAAAAG 240
DB 788 CGAAGAAAAGTCAGTCATGTCTTTTCAGAGGATGAAGCTTAAAGATAAGACTAAAAG 847

QY 241 TGTTCATGCTGGAGTGGAGTGGTATTATATAGGTCTCAGCCCAAGACATGTGATAATC 300
DB 848 TGTTCATGCTGGAGTGGAGTGGTATTATATAGGTCTCAGCCCAAGACATGTGATAATC 907

RESULT 6
AAT95736
ID AAT95736 standard; DNA; 2397 BP.
XX AC AAT95736;
XX DT 13-MAR-1998 (first entry)
XX DE Human tyrosinase gene promoter.
XX KW Pmel17; lambda mel 17-1; ATCC 40264; melanisation; human; melanin;
XX KW melanocyte; biosynthesis; determination; Northern blot analysis;
XX KW probe; tyrosinase; gene promoter; ds.
XX OS Homo sapiens.
XX PN US5679511-A.
XX PD 21-OCT-1997.
XX PF 01-JUN-1992; 92US-0891942.
XX PR 01-JUN-1992; 92US-0891942.
XX PR 06-OCT-1986; 86US-0915753.
XX PR 07-JUN-1989; 89US-0362847.
XX PA (GUTH-) GUTHRIE FOUND MEDICAL RES INC DONALD.
XX PA (INDV ) UNIV INDIANA FOUND.
XX PI Kwon BS;
XX DR WPI; 1997-525715/48.
XX PT Lambda mel 17-1 cDNA and Pmel17 protein - useful as melanin
XX PT biosynthesis probe
XX PS Disclosure; Columns 73-74; 67pp; English.
XX CC The present sequence is disclosed in the specification, which
XX CC describes the isolation of Pmel17, a protein encoded by cDNA
XX CC isolated from lambda mel 17-1 (ATCC 40264). The degree of
XX CC melanisation in a human melanocyte can be determined by subjecting
XX CC human melanocyte RNA to a Northern blot analysis, using the cDNA
XX CC as a probe.
XX SQ Sequence 2397 BP; 808 A; 427 C; 507 G; 655 T; 0 other;
```

```
Query Match 96.3%; Score 289; DB 18; Length 2397;
Best Local Similarity 99.7%; Pred. No. 3.4e-65;
Matches 300; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 TCATTTGCAGGTCAAATCATCATCTAGTTTGTAGTCTATTAACTGGGTTTGCTTAGGTC 60
DB 1926 TCATTTGCAGGTCAAATCATCATCTAGTTTGTAGTCTATTAACTGGGTTTGCTTAGGTC 1985

QY 61 AGGCATTATTATTACTAACTTATTGTTAATATTCTAAACCATAGAACTTAAACCTATTAAAT 120
DB 1986 AGGCATTATTATTACTAACTTATTGTTAATATTCTAAACCATAGAACTTAAACCTATTAAAT 2045

QY 121 GGTGAATAGAGTTTTTCACTTTAACATAGGCCCTATCCCACTGGTGGGATACGAGCCAATT 180
DB 2046 GGTGAATAGAGTTTTTCACTTTAACATAGGCCCTATCCCACTGGTGGGATACGAGCCAATT 2105

QY 181 CGAAG-AAAAGTCAGTCATGCTCTTTTCAGAGGATGAAGCTTAAAGATAAAGACATAAAA 239
DB 2106 CGAAGAAAAGTCAGTCATGCTCTTTTCAGAGGATGAAGCTTAAAGATAAAGACATAAAA 2165

QY 240 GTCTTTGATGCTGGAGTGGGAGTGGTATTATATAGTCTCTACCCCAAGACATCTGATAAT 299
DB 2166 GTCTTTGATGCTGGAGTGGGAGTGGTATTATATAGTCTCTACCCCAAGACATCTGATAAT 2225

QY 300 C 300
DB 2226 C 2226

RESULT 7
AAS63366
ID AAS63366 standard; DNA; 3586 BP.
AC AAS63366;
XX
DT 29-JAN-2002 (first entry)
DE Chemically pretreated metabolism associated gene #61.
KW Human; cytostatic; anti-tumour; metabolism; metabolic disease; liver;
KW solid tumour; cancer; cytosine methylation; epigenetic; eye; kidney;
KW single nucleotide polymorphism detection; SNP; stool; urine; lung;
KW cerebral-spinal fluid; intestine; brain; heart; prostate; breast;
KW DUSP2; EPHX2; QDPR; SGSH; SHMT2; SLC7A4; TYMS; ds.
XX
OS Homo sapiens.
XX
PN WO200176451-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-EP04016.
XX
PR 06-APR-2000; 2000DE-1019058.
PR 07-APR-2000; 2000DE-1019173.
PR 30-JUN-2000; 2000DE-1032529.
PR 01-SEP-2000; 2000DE-1043826.
XX
PA (EPIC-) EPICENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2002-010834/01.
XX
PT New nucleic acid, useful for diagnosis and therapy of metabolic
PT disease, solid tumour and cancers, comprises segment of chemically
PT modified genomic sequences of genes associated with metabolism -
XX
PS Claim 1; Page 140-141; 143pp; English.
XX
CC The invention relates to a nucleic acid (I) comprising a sequence at
CC least 18 bases of a segment of the chemically pretreated DNA of genes
CC associated with metabolism such as DUSP2 (NM_004418), EPHX2 (NM_001979),
```

```
CC QDPR (NM_000320), SGSH (NM_000199), SHMT2 (NM_005412), SLC7A2
CC (NM_003046), SLC7A4 (NM_004173) and TYMS (NM_001071) (all
CC undefined). (I) are useful for diagnosis and therapy of metabolic
CC disease, solid tumours and cancers, as primer oligonucleotides for the
CC amplification of DNA sequences, for detecting the cytosine methylation
CC state and/or single nucleotide polymorphisms (SNPs) in a chemically
CC treated DNA of genes associated with metabolism. An array of (I) is
CC useful for ascertaining genetic and/or epigenetic parameters for the
CC diagnosis and/or therapy of existing diseases or the predisposition to
CC specific diseases by analysing cytosine methylations. The method involves
CC chemically treating genomic DNA sample by a solution of bisulphite,
CC hydrogen sulphite or disulphite such that cytosine bases which are
CC unmethylated at the 5th-position are converted to uracil or another base
CC which is dissimilar to cytosine in terms of hybridisation behaviour and
CC amplifying fragments of the chemically pretreated genomic DNA. The
CC genomic DNA is from cells or cellular components which contain DNA,
CC sources of DNA comprising, for e.g. cell lines, biopsies, blood, sputum,
CC stool, urine, cerebral-spinal fluid, tissue embedded in paraffin such as
CC tissue from eye, intestine, kidney, brain, heart, prostate, lung, breast
CC or liver, histologic object slides and their combinations. Genetic
CC parameters are mutations, in particular insertions, deletions, point
CC mutations, inversions and polymorphisms of genes associated with
CC metabolism and sequences further required for their regulation.
CC Epigenetic parameters are in particular cytosine methylations and
CC further chemical modifications of DNA bases of genes associated with
CC metabolism. Further epigenetic parameters include for e.g. the
CC acetylation of histones which correlates with DNA methylation.
CC AAS63306-AAS63373 represent chemically pretreated metabolism associated
CC genes, and related primers of the invention.
XX
SQ Sequence 3586 BP; 1126 A; 22 C; 761 G; 1677 T; 0 other;

Query Match 78.3%; Score 235; DB 24; Length 3586;
Best Local Similarity 86.6%; Pred. No. 3.2e-51;
Matches 259; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 1 TCATTTGCAGGTCAAATCATCATCTAGTTTGTAGTCTATTAACTGGGTTTGCTTAGGTC 60
DB 608 TTATTTGTAAGGTTAAATATTATTATTAGTTTGTAGTTTATTAACTGGGTTTGCTTAGGTT 667

QY 61 AGGCATTATTATTACTAACTTATTGTTAATATTCTAAACCATAGAACTTAAACCTATTAAAT 120
DB 668 AGGCATTATTATTACTAACTTATTGTTAATATTCTAAACCATAGAACTTAAACCTATTAAAT 727

QY 121 GGTGAATAGAGTTTTTCACTTTAACATAGGCCCTATCCCACTGGTGGGATACGAGCCAATT 180
DB 728 GGTGAATAGAGTTTTTCACTTTAACATAGGCCCTATCCCACTGGTGGGATACGAGCCAATT 787

QY 181 CGAAGAAAAGTCAGTCATGCTCTTTTCAGAGGATGAAGCTTAAAGATAAAGACATAAAA 240
DB 788 CGAAGAAAAGTCAGTCATGCTCTTTTCAGAGGATGAAGCTTAAAGATAAAGACATAAAA 847

QY 241 TGTTTTCATGCTGGAGTGGGAGTGGTATTATATAGTCTCTCAGCCAAGACATGTGATAAT 299
DB 848 TGTTTTCATGCTGGAGTGGGAGTGGTATTATATAGTCTCTCAGCCAAGACATGTGATAAT 906

RESULT 8
AAH43616
ID AAH43616 standard; cDNA; 546 BP.
XX
AC AAH43616;
XX
DT 07-JAN-2002 (first entry)
XX
DE Tyrosinase-TRE.
XX
KW Adenovirus; ADP; replication-competent; adenoviral vector; TRE; PCR;
KW transcriptional regulatory element; mutation; deletion; IRFS; primer;
KW promoter; internal ribosome entry site; cytotoxic; cancer; bladder;
KW amplify; polymerase chain reaction; alpha-fetoprotein; AFP; EMCV;
KW encephalomyocarditis virus; vascular endothelial growth factor; VEGF;
KW immunoglobulin heavy-chain binding protein; BiP; uroplakin II; PDGF;
```

KW platelet derived growth factor; ss.
 OS Homo sapiens.
 XX WO200173093-A2.
 XX 04-OCT-2001.
 XX 21-MAR-2001; 2001WO-US09036.
 XX 24-MAR-2000; 2000US-192156P.
 XX (CALY-) CALYDON INC.
 XX Yu D, Li Y, Henderson DR;
 XX WPI; 2001-639234/73.
 XX Replication-competent adenoviral vector, useful e.g. for killing cancer
 PT cells, contains two genes linked by internal ribosome entry site and
 PT controlled by target-specific regulator.
 XX Example; Page 105-106; 148pp; English.

CC The sequences given in AAH43607-22 represent sequences which may be used
 CC in the replication-competent adenoviral vector (A) of the invention.
 CC The vector contains two genes (G1, G2) that are co-transcribed as a
 CC single mRNA and under control of a heterologous, target cell-specific
 CC transcriptional regulatory element (TRE). G2 has a mutation in, or
 CC deletion of, its endogenous promoter and is controlled from an internal
 CC ribosome entry site (IRES). (A) has greater specificity for a target
 CC cell than a similar vector in which TRE is operably linked to a gene
 CC and which lacks an IRES. (A) are used to modify the genotype of target
 CC cells, optionally in vitro with subsequent return of altered cells to
 CC the host and where G2 is a cytotoxic gene, to confer selective cyto-
 CC toxicity to target cells, especially for killing cancer cells. Also
 CC (A) are used for diagnosis and monitoring, e.g. detection of bladder
 CC cancer cells. The target cell-specific TRE ensures that (A) has better
 CC targeting specificity, with minimal replication in non-target cells, so
 CC a runaway infection is prevented but production of adenoviral proteins
 CC in target cells activates and/or stimulates the immune response against
 CC target cells producing such proteins. The use of an IRES (rather than
 CC two identical control elements) eliminates the risk of homologous
 CC recombination and may provide enough extra space for an additional
 CC (therapeutic) gene.

XX Sequence 546 BP; 176 A; 96 C; 122 G; 152 T; 0 other;

Query Match 73.0%; Score 219; DB 22; Length 546;
 Best Local Similarity 99.6%; Pred. No. 3e-47;
 Matches 230; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 71 ATTACTAACCTTATTTCTTAATTTCTTAACCATTAAGAAATTAACCTATTATTTGTTGAATAGA 130
 DB 251 ATTACTAACCTTATTTCTTAATTTCTTAACCATTAAGAAATTAACCTATTATTTGTTGAATAGA 310
 QY 131 GTTTTTCACCTTTAAACATAGCCCTATCCCACTGGTGGGATACGAGCAATTCGAAAG-AAA 189
 DB 311 GTTTTTCACCTTTAAACATAGCCCTATCCCACTGGTGGGATACGAGCAATTCGAAAGAAAA 370
 QY 190 AGTCAGTCATGCTTTTTCAGAGGATGAAGCTTAAAGACTTAAGACTTAAGACTTAAGACTTAAG 249
 DB 371 AGTCAGTCATGCTTTTTCAGAGGATGAAGCTTAAAGACTTAAGACTTAAGACTTAAGACTTAAG 430
 QY 250 CTGAGGTGGGAGTGGTATTATATAGTCTCAGCCCAAGACATGTGATAATC 300
 DB 431 CTGAGGTGGGAGTGGTATTATATAGTCTCAGCCCAAGACATGTGATAATC 481

RESULT 9
 ID AAF87236
 XX AAF87236 standard; DNA; 546 BP.

AC AAF87236;
 XX 26-MAR-2002 (first entry)
 XX Tyrosinase-TRE fusion protein coding sequence.
 XX Tumour growth suppression; adenovirus vector; antineoplastic agent;
 KW transcriptional regulatory element; TRE; radiotherapy; bladder cancer;
 KW prostate cancer; liver cancer; breast cancer; colon cancer; melanoma;
 KW ovarian cancer; pancreatic cancer; lung cancer; brain cancer; therapy;
 KW Tyrosinase-TRE; ds.
 XX Homo sapiens.
 XX WO200172341-A2.
 XX 04-OCT-2001.
 XX 21-MAR-2001; 2001WO-US09042.
 XX 24-MAR-2000; 2000US-192015P.
 XX (CALY-) CALYDON INC.
 XX Yu D, Chen Y, Henderson DR;
 XX WPI; 2001-648426/74.
 XX Suppression of tumour growth, e.g. liver, bladder or breast cancer,
 PT comprises using a synergistic combination of adenovirus vector and
 PT antineoplastic agent or radiotherapy.
 XX Claim 12; Page 174; 248pp; English.

XX This sequence represents a Tyrosinase-TRE fusion protein coding sequence
 CC used in the scope of the invention. The invention relates to a method
 CC for the suppression of tumour growth comprising the administration of:
 CC (a) a target cell-specific adenovirus vector comprising an adenoviral
 CC gene essential for replication under transcriptional control of a
 CC target cell-specific transcriptional regulatory element (TRE); and
 CC (b) at least one antineoplastic agent; or (c) a course of radiotherapy
 CC where the amount of (a) and/or (b) or (c) is lower than that known to be
 CC effective for suppressing tumour growth when administered alone.
 CC The method is used for suppression of tumour growth for treatment of
 CC e.g. bladder cancer, prostate cancer, liver cancer, breast cancer, colon
 CC cancer, melanoma, ovarian cancer, pancreatic cancer, lung cancer or brain
 CC cancer. The combinations enhance the efficacy of treatment, allowing
 CC lower doses to be administered, reducing toxicity and suffering of the
 CC patient.

XX Sequence 546 BP; 176 A; 96 C; 122 G; 152 T; 0 other;

Query Match 73.0%; Score 219; DB 23; Length 546;
 Best Local Similarity 99.6%; Pred. No. 3e-47;
 Matches 230; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 71 ATTACTAACCTTATTTCTTAATTTCTTAACCATTAAGAAATTAACCTATTATTTGTTGAATAGA 130
 DB 251 ATTACTAACCTTATTTCTTAATTTCTTAACCATTAAGAAATTAACCTATTATTTGTTGAATAGA 310
 QY 131 GTTTTTCACCTTTAAACATAGCCCTATCCCACTGGTGGGATACGAGCAATTCGAAAG-AAA 189
 DB 311 GTTTTTCACCTTTAAACATAGCCCTATCCCACTGGTGGGATACGAGCAATTCGAAAGAAAA 370
 QY 190 AGTCAGTCATGCTTTTTCAGAGGATGAAGCTTAAAGACTTAAGACTTAAGACTTAAGACTTAAG 249
 DB 371 AGTCAGTCATGCTTTTTCAGAGGATGAAGCTTAAAGACTTAAGACTTAAGACTTAAGACTTAAG 430
 QY 250 CTGAGGTGGGAGTGGTATTATATAGTCTCAGCCCAAGACATGTGATAATC 300
 DB 431 CTGAGGTGGGAGTGGTATTATATAGTCTCAGCCCAAGACATGTGATAATC 481

RESULT 10
 AAS63367/C
 ID AAS63367 standard; DNA; 3586 BP.
 XX
 AC AAS63367;
 XX
 DT 29-JAN-2002 (first entry)
 XX
 DE Chemically pretreated metabolism associated gene #62.
 XX
 KW Human: cytostatic; anti-tumour; metabolism; metabolic disease; liver;
 KW solid tumour; cancer; cytosine methylation; epigenetic; eye; kidney;
 KW single nucleotide polymorphism detection; SNP; stool; urine; lung;
 KW cerebral-spinal fluid; intestine; brain; heart; prostate; breast;
 KW DUSP2; EPHX2; QDPR; SGSH; SHMT2; SLC7A2; SLC7A4; TYMS; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200176451-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-EP04016.
 XX
 PR 06-APR-2000; 2000DE-1019058.
 PR 07-APR-2000; 2000DE-1019173.
 PR 30-JUN-2000; 2000DE-1032529.
 PR 01-SEP-2000; 2000DE-1043826.
 XX
 PA (EPIC-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2002-010834/01.
 XX
 PT New nucleic acid, useful for diagnosis and therapy of metabolic
 PT disease, solid tumour and cancers, comprises segment of chemically
 PT modified genomic sequences of genes associated with metabolism -
 XX
 PS Claim 1; Page 141-142; 143pp; English.
 XX
 CC The invention relates to a nucleic acid (I) comprising a sequence at
 CC least 18 bases of a segment of the chemically pretreated DNA of genes
 CC associated with metabolism such as DUSP2 (NM_004418), EPHX2 (NM_001979),
 CC QDPR (NM_000320), SGSH (NM_000199), SHMT2 (NM_005412), SLC7A2
 CC (NM_003046), SLC7A4 (NM_004173) and TYMS (NM_001071) (all
 CC undefined). (I) are useful for diagnosis and therapy of metabolic
 CC disease, solid tumours and cancers; as primer oligonucleotides for the
 CC amplification of DNA sequences, for detecting the cytosine methylation
 CC state and/or single nucleotide polymorphisms (SNPs) in a chemically
 CC treated DNA of genes associated with metabolism. An array of (I) is
 CC useful for ascertaining genetic and/or epigenetic parameters for the
 CC diagnosis and/or therapy of existing diseases or the predisposition to
 CC specific diseases by analysing cytosine methylations. The method involves
 CC chemically treating genomic DNA sample by a solution of bisulphite,
 CC hydrogen sulphite or disulphite such that cytosine bases which are
 CC unmethylated at the 5th-position are converted to uracil or another base
 CC which is dissimilar to cytosine in terms of hybridisation behaviour and
 CC amplifying fragments of the chemically pretreated genomic DNA. The
 CC genomic DNA is from cells or cellular components which contain DNA,
 CC sources of DNA comprising, for e.g. cell lines, biopsies, blood, sputum,
 CC stool, urine, cerebral-spinal fluid, tissue embedded in paraffin such as
 CC tissue from eye, intestine, kidney, brain, heart, prostate, lung, breast
 CC or liver, histologic object slides and their combinations. Genetic
 CC parameters are mutations, in particular insertions, deletions, point
 CC mutations, inversions and polymorphisms of genes associated with
 CC metabolism and sequences further required for their regulation.
 CC Epigenetic parameters are in particular cytosine methylations and
 CC further chemical modifications of DNA bases of genes associated with
 CC metabolism. Further epigenetic parameters include for e.g. the
 CC acetylation of histones which correlates with DNA methylation.
 CC AAS63306-AAS63373 represent chemically pretreated metabolism associated
 CC genes, and related primers of the invention.

XX
 SQ Sequence 3586 BP; 1063 A; 22 C; 636 G; 1865 T; 0 other;
 Query Match 67.5%; Score 202.4; DB 24; Length 3586;
 Best Local Similarity 79.7%; Pred. No. 8.5e-43;
 Matches 239; Conservative 0; Mismatches 61; Indels 0; Gaps 0;
 QY 1 TCATTTCGCAAGTCAAAATCATCATCTAGTTTGTAGTCTATTAACTGGTTTCTTAGGTC 60
 DB 2979 TCATTTCGCAAAATCAATCATCATCTAGTTTGTAGTCTATTAACTGGTTTCTTAGGTC 2920
 QY 61 AGCATTATTATTACAACTTATTTGTTATATTTCAACCATAGAAATTAATCTATTAT 120
 DB 2919 AAACATTATTATTACAACTTATTTGTTATATTTCAACCATAGAAATTAATCTATTAT 2860
 QY 121 GGTGAATAGAGTTTTCACCTTTAAACATAGCCCTATCCCACTGGTGGATACGAGCCAATT 180
 DB 2859 AATAAATAAATTTTCACCTTTAAACATAGCCCTATCCCACTGGTGGATACGAGCCAATT 2800
 QY 181 CGAAGAAAAGTCAGTCATGTGCTTTTCAGAGGATGAAAGCTTTAAGATAAAGACTAAAG 240
 DB 2799 CGAAGAAAAGTCAATCATATACCTTTTCAAAAAATAAAACTTTAAAAATAAACTAAAAA 2740
 QY 241 TGTTTCATGCTGGAGGTGGAGTGGTATTATATAGTCTCAGCCAGACATGTGATATTC 300
 DB 2739 TATTTAATACTAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATC 2680
 RESULT 11
 AAS63367 standard; DNA; 4752 BP.
 ID AAS63367 standard; DNA; 4752 BP.
 XX
 AC AAS63367;
 XX
 DT 01-AUG-1994 (first entry)
 XX
 DE Tyrosinase promoter.
 XX
 KW Tyrosinase; cytokine; tumor therapy; gene therapy; melanoma;
 KW B16; tumor-specific promoter; polymerase chain reaction; PCR;
 KW B16; primer; ds.
 XX
 OS Mus sp.
 XX
 PN WO9404196-A.
 XX
 PD 03-MAR-1994.
 XX
 PF 16-AUG-1993; 93WO-GB01730.
 XX
 PR 14-AUG-1992; 92GB-0017270.
 PR 27-FEB-1993; 93GB-0004024.
 XX
 XX (IMCR) IMPERIAL CANCER RES TECHNOLOGY.
 PA
 PI Hart IR, Vile RG;
 XX
 DR WPI; 1994-082848/10.
 XX
 PT DNA construct encoding cytokine for expression in tumour cells -
 PT for treating melanoma, pancreatic, breast, colon, prostate cancer
 XX
 PS Disclosure; Page 67-70; 107pp; English.
 XX
 CC Cytokine genes are expressed in tumor cells, especially melanoma
 CC cells, under the control of the tumor-specific tyrosinase gene
 CC promoter, for gene therapy. A DNA fragment from the 5' end of
 CC the tyrosinase gene was generated by PCR from genomic DNA of the
 CC B16 melanoma line using the primers given in AAS63041-46.
 XX
 SQ Sequence 4752 BP; 1550 A; 854 C; 883 G; 1465 T; 0 other;
 Query Match 22.3%; Score 67; DB 15; Length 4752;

Sequences AAS45296-AAS45520 represent chemically pretreated genomic DNA molecules associated with the cell cycle and specific PCR primers of the invention. The sequences are useful for detecting the methylation state of all CpG dinucleotides in a sequence and therefore for analysing associated diseases. By analysing cytosine methylations in the pretreated DNA, genetic and/or epigenetic parameters for the diagnosis and therapy of existing diseases or the predisposition to specific diseases can be ascertained. The parameters may be compared to another set of genetic and/or epigenetic parameters, the differences serving as basis for diagnosis and/or prognosis events which are disadvantageous to patients. The sequences of the invention are useful for the diagnosis and therapy of HIV infection, neurodegenerative disorders, graft-versus-host disease, aging, glomerular disease, Lewy body disease, arthritis, arteriosclerosis, solid tumours and cancers.

Seq	Sequence	7195 bp;	2059 A;	224 C;	1725 G;	3187 T;	0 other;	
Query Match	13.6%;	Score	40.8;	DB	22;	Length	7195;	
Best Local Similarity	48.3%;	Pred. No.	0.52;					
Matches	114;	Conservative	0;	Mismatches	122;	Indels	0;	Gaps
Qy	13	TCAAATCATATAGTTTTGTAGTCTATTAACTGGGTTTGGCTTAGGTCAGGCATTATTAT	72					
Db	2750	TTAAAGTGTATTGGTTTGAAGATTTTATATTTTGTGTAGTATGTCGCTTTT	2809					
Qy	73	TACTAACCTTATTGTTTAATATCTTAACCATAAGAAATTAACATATTAAATGGTCAATAGAGT	132					
Db	2810	TTTTTAGTTTAAAAATAAATTTAGTTGAAAAGCTAATAATAATTTATGTTATATAGATT	2869					
Qy	133	TTTTCACCTTTAAACATAGGCTATCCCACTGGTGGGATACGAGCCCAATTCGAAGAAAGCT	192					
Db	2870	AATAATAAAAATAAGAAGGTAATTTGTTGGTGTAGATATTGTAATTAAGTTAAATAAGT	2929					
Qy	193	CAGTCATGTGCTCTTTCAGAGGATGAAGAGCTTTAAGATAAAGACTAAAAAGCTGTTTGGAT	248					
Db	2930	AATTTTGTGTAAATATTGAAGTAAGTGTCTTTGAAGAAATTTTAAAGCAATTTTAAAGCTTTATAGT	2985					

RESULT 14	
ABK28165	
ID	ABK28165 standard: DNA; 7195 BP.
XX	
AC	ABK28165;
XX	
DT	23-APR-2002 (first entry)
XX	
DE	DNA transcription associated genomic DNA #20.
XX	
XX	DNA transcription associated gene; peptide nucleic acid; PNA-oligomer;
KW	PNA; cytosine methylation state; SNP; retroviral infection; gene; ds;
KW	single nucleotide polymorphism; adenosine deaminase deficiency; cancer;
KW	viral infection; Sezary syndrome; haematological disorder; tuberculosis;
KW	immunological disorder; Werner syndrome; developmental disorder;
KW	psoriasis; Rieger's syndrome; neurological disorder; erythropoiesis;
KW	neurodegenerative disorder; Waardenburg syndrome; Niemann-Pick disease;
KW	myelodysplastic syndrome; myocardial infarction; hypertension; arthritis;
KW	angiogenesis; congenital heart disease; HDR syndrome; gene therapy;
KW	polylutamine disorder; solid tumour

XX	Unidentified.
OS	
XX	WO200192565-A2.
PN	
XX	06-DEC-2001.
PD	
XX	06-APR-2001; 2001WO-EP03973.
PF	
XX	
PR	06-APR-2000; 2000DE-1019058.
PR	07-APR-2000; 2000DE-1019173.
PR	30-JUN-2000; 2000DE-1032529.
PR	01-SEP-2000; 2000DE-1043826.
XX	
XX	

PA (EPIG-) EPIGENOMICS AG.

PI Olek A, Piepenbrock C, Berlin K;
XX

XX
DR WPI: 2002-090046/12.

XX New nucleic acids or oligomers, useful for diagnosing or treating
PT diseases associated with DNA transcription, e.g. immunological
PT disorders, Werner syndrome, psoriasis, myocardial infarction, sol
PT tumours or cancer

XX
PS Claim 1: SEO ID No 39; 32pp; English.

The invention relates to a nucleic acid, which comprises a segment of the chemically pretreated DNA of genes associated with DNA transcription from one of 346 sequences, and an oligomer, in particular an oligonucleotide or peptide nucleic acid (PNA)-oligomer that hybridises to or is identical to the chemically pretreated DNA of genes associated with DNA transcription. The set of oligomer probes are useful for detecting the cytosine methylation state and/or single nucleotide polymorphisms (SNPs) in a chemically pretreated genomic DNA. The nucleic acids are useful for diagnosing or treating diseases associated with DNA transcription (particularly with the methylation status), e.g. adenosine deaminase deficiency, viral infection, retroviral infection, Sezary syndrome, haematological disorders, immunological disorders, Werner syndrome, tuberculosis, developmental disorders, psoriasis, Rieger's syndrome, neurological disorders, neurodegenerative disorders, Waardenburg syndrome, Niemann-Pick disease, myelodysplastic syndrome, myocardial infarction, hypertension, angiogenesis, erythropoiesis, congenital heart disease, HDR syndrome, arthritis, polyglutamine disorders, solid tumours or cancer. Sequences ABK28127-ABK28472 represent DNA transcription associated genomic DNA molecules of the invention.

CC associated genomic DNA molecules of the invention.
CC Note: The sequence data for this patent did not form:part of the printed
CC specification but was obtained in electronic format directly from the
CC European Patent Office.

Sequence 7195 BP; 2059 A; 224 C; 1725 G; 3187 T; 0 other;

Query Match	13.6%	Score 40.8;	DB 24;	Length 7195;
Best Local Similarity	48.3%	Pred. NO. 0.52;		
Matches 114;	Conservative	0;	Mismatches 122;	Indels 0;
				Gaps 0;

Qy	13	TCAAAATCATATTAGTTTGTCTAGCTATTAACTGGGTTTGGCTTACGTCAGGCATATTAT	72
Db	2750	TTAAATCTTTATTTGGTTTACAAATTTATTATTTTGTGTAGTATTATGTCGCTTTT	2809
Qy	73	TACTAACCTTATTGTGTTTAATCTCAACCATAGAAATTAACACTATTAAATGGTCAATAGAGT	132
Db	2810	TTTTTAGTTTAAATAAATTTAGTGTGAAAGTAATAATAAATTTATTATGTATATAGATT	2869
Qy	133	TTTTCACTTTAAACATAGGCCATCCACCTGGTGGGATACGAGCCCAATTCGAAAGAAAGT	192
Db	2870	AATAAATAAATAAGAGGTAAATTTGTTGGCTGTAGATATTGTAATAAGTTAAATAAGT	2929
Qy	193	CAGTCATGCTGCTTTTCAGAGGATGAAGGCTTAAGATAAAGACATAAAGCTGTTTCAAT	248
Db	2930	AATTTTTGCTAAATATTGAAGTAAGTGTTTGAAGAAATTTATAAAGATTTATATCAT	2985

RESULT 15

AAS60958
ID AAS60958 standard: CDNA: 2041 BP.

XX
AC AAS60958;

XX
DT 29-JAN-2002 (first entry).

XX Human cancer agent-resistance marker #617. DE

XX	Human: cancer cell marker; TAXOL; cytostatic; tumour; carcinoma
KW	squamous cell carcinoma; sarcoma; fibrosarcoma; leukaemia;
KW	lymphocytic leukaemia; lymphoma; plasmacytoma; reticulum cell sarcoma
KW	Hodgkin's disease; glioma; ss.

```
XX OS Homo sapiens.
XX PN WO200179556-A2.
XX PD 25-OCT-2001.
XX PF 13-APR-2001; 2001WO-US12132.
XX PR 14-APR-2000; 2000US-197538P.
XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX PI Lillie J, Brown JL, Bolt A, Van Huffel C;
XX DR WPI; 2001-602933/68.
XX PT Novel nucleic acid, used as a marker to determine the effectiveness of
XX using TAXOL to treat cancer cell growth in individuals -
XX PS Claim 1; Page 460-461; 527pp; English.
XX The invention relates to 1046 novel nucleic acids which are used as
CC markers for determining the sensitivity of a cancer cell to the
CC anticancer agent TAXOL. Cancer cells can be treated with TAXOL when
CC they are shown to express one of the 242 sensitivity markers or the
CC cells are shown not to express one of the 804 resistance markers.
CC The methods can be used to determine the effectiveness of TAXOL
CC in the treatment of cancer cell growth in an individual. The markers
CC can be used as targets in developing anti-cancer agents such as
CC chemotherapeutic compounds. The markers can also be used as targets in
CC developing treatments for cancer, particularly those cancers which
CC display resistance to agents and exhibit expression of the markers. The
CC anticancer agents developed by the novel method can be used to treat
CC cancer. Probes based on the markers can be used to detect transcripts or
CC genomic sequences corresponding to the markers, in the identification of
CC cells or tissues which mis-express the protein. Cancers which may
CC be targeted include carcinoma (e.g. squamous cell carcinoma),
CC sarcoma (e.g. fibrosarcoma) leukaemia (e.g. lymphocytic leukaemia),
CC lymphoma, plasmocytoma, reticulum cell sarcoma, Hodgkin's disease and
CC tumours (e.g. glioma). The present sequence is one of the 1046
CC novel cancer cell markers.
XX SQ Sequence 2041 BP; 564 A; 467 C; 455 G; 548 T; 7 other;

Query Match 13.3%; Score 40; DB 22; Length 2041;
Best Local Similarity 100.0%; Pred. No. 0.65;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 261 ACTGGTATTATAGTCTCAGCCAGACATGTGATAATC 300
Db 7 ACTGGTATTATAGTCTCAGCCAGACATGTGATAATC 46

Search completed: May 10, 2003, 16:18:04
Job time : 273 secs
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OM nucleic - nucleic search, using sw model

Run on: May 10, 2003, 16:13:41 ; Search time 70 Seconds
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Title: US-09-721-391-1

Perfect score: 300

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:**
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	300	100.0	2384	1 US-08-181-471-1	Sequence 1, Appli
2	300	100.0	2384	4 US-09-056-105-3	Sequence 3, Appli
3	289	96.3	2397	1 US-07-891-942G-11	Sequence 11, Appli
C 4	34.6	11.5	1001	4 US-09-641-638-377	Sequence 377, App
C 5	34.2	11.4	1725	4 US-09-134-001C-2572	Sequence 2572, Ap
6	34.2	11.4	3155	2 US-08-591-629-7	Sequence 7, Appli
7	33.8	11.3	1512	4 US-09-134-001C-1111	Sequence 1111, Ap
C 8	33.4	11.1	1001	4 US-09-641-638-376	Sequence 376, App
9	32.4	10.8	334	2 US-09-032-684-8	Sequence 8, Appli
10	32.2	10.7	2048	1 US-08-416-870C-7	Sequence 7, Appli
11	32.2	10.7	3696	2 US-08-657-641-4	Sequence 4, Appli
12	32.2	10.7	3696	5 PCT-US94-07233-4	Sequence 4, Appli
C 13	32.2	10.7	5303	4 US-08-971-395-4	Sequence 4, Appli
14	32	10.7	2476	4 US-08-844-274-11	Sequence 11, Appl
15	32	10.7	4198	4 US-09-586-719-11	Sequence 11, Appl
16	32	10.7	5194	4 US-08-844-274-16	Sequence 16, Appl
17	32	10.7	5194	4 US-08-844-274-17	Sequence 17, Appl
C 18	32	10.7	5679	4 US-08-844-274-10	Sequence 10, Appl
19	32	10.7	6448	4 US-08-844-274-15	Sequence 15, Appl
C 20	32	10.7	6723	4 US-08-844-274-13	Sequence 13, Appl
21	32	10.7	6723	4 US-08-844-274-14	Sequence 14, Appl
22	32	10.7	7560	4 US-08-844-274-20	Sequence 20, Appl
C 23	31.8	10.6	9060	4 US-08-378-313-20	Sequence 20, Appl
24	31.8	10.6	84495	4 US-09-797-906-3	Sequence 3, Appli
C 25	31.6	10.5	263	3 US-08-765-332-144	Sequence 144, App
C 26	31.6	10.5	263	4 US-09-448-894-144	Sequence 144, App
C 27	31.6	10.5	2237	4 US-08-914-999-7	Sequence 7, Appli

28	31.4	10.5	4285	4 US-09-410-464-1	Sequence 1, Appli
C 29	31.4	10.5	8920	2 US-08-446-855A-1	Sequence 1, Appli
C 30	31.4	10.5	8920	4 US-09-150-741-1	Sequence 1, Appli
C 31	31.2	10.4	4291	2 US-08-417-210A-81	Sequence 81, Appli
32	31	10.3	750	2 US-08-687-080-74	Sequence 74, Appli
C 33	31	10.3	1546	3 US-08-961-083-21	Sequence 21, Appli
C 34	31	10.3	6854	4 US-09-066-047-6	Sequence 200, App
C 35	30.8	10.2	4285	4 US-09-410-464-1	Sequence 1, Appli
C 36	30.6	10.2	4285	4 US-09-066-047-6	Sequence 6, Appli
C 37	30.6	10.2	5300	1 US-08-766-014-1	Sequence 1, Appli
38	30.6	10.2	6124	4 US-08-213-419B-3	Sequence 3, Appli
C 39	30.6	10.2	12571	4 US-09-322-478-20	Sequence 20, Appli
C 40	30.4	10.1	7336	4 US-09-306-446C-1	Sequence 1, Appli
C 41	30.2	10.1	1524	4 US-09-134-001C-2234	Sequence 2234, Ap
42	30.2	10.1	1680	4 US-08-961-527-270	Sequence 270, App
C 43	30	10.0	30	4 US-09-150-766-14	Sequence 14, Appli
44	30	10.0	211	1 US-07-593-657-12	Sequence 12, Appli
45	30	10.0	1388	1 US-08-282-581-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-08-181-471-1
: Sequence 1, Application US/08181471
: Patent No. 5641508
: GENERAL INFORMATION:
: APPLICANT: Li, Lingna
: APPLICANT: Lishko, Valeryi K.
: TITLE OF INVENTION: METHOD FOR DELIVERING BENEFICIAL
: TITLE OF INVENTION: COMPOSITIONS TO HAIR FOLLICLES
: NUMBER OF SEQUENCES: 3
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Thomas Fitting
: STREET: 13526 High Bluff Drive, Suite 300
: CITY: San Diego
: STATE: CA
: COUNTRY: USA
: ZIP: 92130
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/181,471
: FILING DATE: 13-JAN-1994
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/041,553
: FILING DATE: 02-APR-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Fitting, Thomas
: REGISTRATION NUMBER: 34,163
: REFERENCE/DOCKET NUMBER: ANT0029P
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 619-792-3680
: TELEFAX: 619-792-8477
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2384 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: CDNA
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 503..2092
US-08-181-471-1

Query Match 100.0%; Score 300; DB 1; Length 2384;
Best Local Similarity 100.0%; Pred. No. 2.7e-77;
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCATTGCAAGGTCAAAATCATCATAGTTTGTAGTCTATTAACTGGGTTGCTTAGGTC 60
DB 124 TCATTGCAAGGTCAAAATCATCATAGTTTGTAGTCTATTAACTGGGTTGCTTAGGTC 183
QY 61 AGGCATTATTACTAACCTTATTGTTAAATTTCTAACCATTAAGAAATAAATTAAT 120
DB 184 AGGCATTATTACTAACCTTATTGTTAAATTTCTAACCATTAAGAAATAAATTAAT 243
QY 121 GGTGAATAGAGTTTTCACCTTAAACATAGGCTATCCCACTGGTGGGATACAGCAATT 180
DB 244 GGTGAATAGAGTTTTCACCTTAAACATAGGCTATCCCACTGGTGGGATACAGCAATT 303
QY 181 CGAAGAAAAGTCAGTCATGTCTTTTCAGAGGATGAAAGCTTAAGATAAAGACTAAAAG 240
DB 304 CGAAGAAAAGTCAGTCATGTCTTTTCAGAGGATGAAAGCTTAAGATAAAGACTAAAAG 363
QY 241 TGTGATGCTGGAGGTGGAGTGGTATTATATAGGCTCTCAGCCAAAGACATGTGATAATC 300
DB 364 TGTGATGCTGGAGGTGGAGTGGTATTATATAGGCTCTCAGCCAAAGACATGTGATAATC 423

RESULT 2
US-09-056-105-3
; Sequence 3, Application US/09056105
; Patent No. 6287569
; GENERAL INFORMATION:
; APPLICANT: KIPPS, THOMAS J.
; APPLICANT: WU, YUNQI
; TITLE OF INVENTION: VACCINES WITH ENHANCED INTRACELLULAR
; FILE REFERENCE: 233/221
; CURRENT APPLICATION NUMBER: US/09/056.105
; CURRENT FILING DATE: 1998-04-06
; EARLIER FILING DATE: 1997-04-10
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 2384
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-056-105-3

Query Match 100.0%; Score 300; DB 4; Length 2384;
Best Local Similarity 100.0%; Pred. No. 2.7e-77;
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCATTGCAAGGTCAAAATCATCATAGTTTGTAGTCTATTAACTGGGTTGCTTAGGTC 60
DB 124 TCATTGCAAGGTCAAAATCATCATAGTTTGTAGTCTATTAACTGGGTTGCTTAGGTC 183
QY 61 AGGCATTATTACTAACCTTATTGTTAAATTTCTAACCATTAAGAAATAAATTAAT 120
DB 184 AGGCATTATTACTAACCTTATTGTTAAATTTCTAACCATTAAGAAATAAATTAAT 243
QY 121 GGTGAATAGAGTTTTCACCTTAAACATAGGCTATCCCACTGGTGGGATACAGCAATT 180
DB 244 GGTGAATAGAGTTTTCACCTTAAACATAGGCTATCCCACTGGTGGGATACAGCAATT 303
QY 181 CGAAGAAAAGTCAGTCATGTCTTTTCAGAGGATGAAAGCTTAAGATAAAGACTAAAAG 240
DB 304 CGAAGAAAAGTCAGTCATGTCTTTTCAGAGGATGAAAGCTTAAGATAAAGACTAAAAG 363
QY 241 TGTGATGCTGGAGGTGGAGTGGTATTATATAGGCTCTCAGCCAAAGACATGTGATAATC 300
DB 364 TGTGATGCTGGAGGTGGAGTGGTATTATATAGGCTCTCAGCCAAAGACATGTGATAATC 423

RESULT 3

US-07-891-942G-11
; Sequence 11, Application US/07891942G
; Patent No. 5679511
; GENERAL INFORMATION:
; APPLICANT: Kwon, Byoung Se
; TITLE OF INVENTION: CDNA CLONES FOR HUMAN TYROSINASE AND FOR
; TITLE OF INVENTION: A REGULATORY PROTEIN IN THE MELANIN PROTEIN PATHWAY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Christopher A. Michaels, Barnard, Brown &
; ADDRESSEE: Michaels
; STREET: 306 East State Street; Suite 220
; CITY: Ithaca
; STATE: NY
; COUNTRY: USA
; ZIP: 14850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/891,942G
; FILING DATE: 01-JUN-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 06/915,753
; FILING DATE: 06-OCT-1986
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/362,847
; FILING DATE: 07-JUN-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Michaels, Christopher A
; REGISTRATION NUMBER: 34,390
; REFERENCE/DOCKET NUMBER: IND1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 607-273-1711
; TELEFAX: 607-273-2609
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2397 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-07-891-942G-11

Query Match 96.3%; Score 289; DB 1; Length 2397;
Best Local Similarity 99.7%; Pred. No. 3.9e-74;
Matches 300; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 TCATTGCAAGGTCAAAATCATCATAGTTTGTAGTCTATTAACTGGGTTGCTTAGGTC 60
DB 1926 TCATTGCAAGGTCAAAATCATCATAGTTTGTAGTCTATTAACTGGGTTGCTTAGGTC 1985
QY 61 AGGCATTATTACTAACCTTATTGTTAAATTTCTAACCATTAAGAAATAAATTAAT 120
DB 1986 AGGCATTATTACTAACCTTATTGTTAAATTTCTAACCATTAAGAAATAAATTAAT 2045
QY 121 GGTGAATAGAGTTTTCACCTTAAACATAGGCTATCCCACTGGTGGGATACAGCAATT 180
DB 2046 GGTGAATAGAGTTTTCACCTTAAACATAGGCTATCCCACTGGTGGGATACAGCAATT 2105
QY 181 CGAAG-AAAAGTCAGTCATGTCTTTTCAGAGGATGAAAGCTTAAGATAAAGACTAAA 239
DB 2106 CGAAGAAAAGTCAGTCATGTCTTTTCAGAGGATGAAAGCTTAAGATAAAGACTAAA 2165
QY 240 GTGTTTGTGCTGGAGGTGGAGTGGTATTATATAGGCTCTCAGCCAAAGACATGTGATAAT 299
DB 2166 GTGTTTGTGCTGGAGGTGGAGTGGTATTATATAGGCTCTCAGCCAAAGACATGTGATAAT 2225
QY 300 C 300

RESULT 10
US-08-416-870C-7
; Sequence 7, Application US/08416870C
; Patent No. 5824862
; GENERAL INFORMATION:

```

RESULT 11
US-08-657-641-4
; Sequence 4, Application US/08657641
; Patent No. 5945277
; GENERAL INFORMATION:
; APPLICANT: Nichol, Stuart T.
; APPLICANT: Spiropoulos, Christl
; APPLICANT: Ksiazek, Thomas G.
; APPLICANT: Rollin, Pierre E.
; TITLE OF INVENTION: NUCLEIC ACID
; TITLE OF INVENTION: AND
; TITLE OF INVENTION: REAGENTS F(
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Suite 1200, The Ca
; STREET: 127 Peachtree Street,

```

CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30303-1811
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/657,641
FILING DATE: 24-JUN-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/133,591
FILING DATE: 07-OCT-1993
APPLICATION NUMBER: US 1414,074
FILING DATE: 24-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Perryman, David G.
REGISTRATION NUMBER: 33,438
REFERENCE/DOCKET NUMBER: 1414,089
TELEPHONE: 404-688-9870
TELEFAX: 404-688-9880
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 3696 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Nucleic Acid
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Hantavirus
STRAIN: New
POSITION IN GENOME:
CHROMOSOME/SEGMENT: M Segment
UNITS: 3696 BP
US-08-657-641-4

Query Match 10.7% Score 32.2; DB 2; Length 3696;
Best Local Similarity 49.1%; Pred. No. 3;
Matches 85; Conservative 0; Mismatches 88; Indels 0; Gaps 0;
QY 8 CAAGGTCAAAATCATCATAGTTTGTCTTACTTATTAACCTGGGTTTCTTAGGTACGGCATT 67
DB 3502 CAACATTATTTCATTATATGTATGTCTTATATCAATAACATTTGTATATATCCCATACC 3561
QY 68 ATTATTACTAACCTTATTGTTTAATTTCTAACCATTAAGAAATTAACCTTATTATGTTGAAT 127
DB 3562 GAAATATTATTAATAATTTTATTTTATACAAAGTATTAACTAACCCATTAAACAGCTAAA 3621
QY 128 AGAGTTTTTTCACCTTTAAACATAGGCTATCCCACTGGTGGATACAGCAATT 180
DB 3622 AAAACAATCCTTAACACCTATATATATCCCATTTGCTTATTACGAGCTTTT 3674

RESULT 12
PCT-US94-07233-4
Sequence 4, Application PC/TUS9407233
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: NUCLEIC ACIDS OF A NOVEL HANTAVIRUS AND REAGENTS FOR DETECTION
NUMBER OF SEQUENCES: 12
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07233

FILING DATE: 24-JUN-94
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/084,724
FILING DATE: 24-JUN-1993
APPLICATION NUMBER: US 08/591,133
FILING DATE: 07-OCT-1993
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 3696 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Nucleic Acid
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Hantavirus
STRAIN: New
POSITION IN GENOME:
CHROMOSOME/SEGMENT: M Segment
UNITS: 3696 BP
PCT-US94-07233-4
Query Match 10.7% Score 32.2; DB 5; Length 3696;
Best Local Similarity 49.1%; Pred. No. 3;
Matches 85; Conservative 0; Mismatches 88; Indels 0; Gaps 0;
QY 8 CAAGGTCAAAATCATCATAGTTTGTCTTACTTATTAACCTGGGTTTCTTAGGTACGGCATT 67
DB 3502 CAACATTATTTCATTATATGTATGTCTTATATCAATAACATTTGTATATATCCCATACC 3561
QY 68 ATTATTACTAACCTTATTGTTTAATTTCTAACCATTAAGAAATTAACCTTATTATGTTGAAT 127
DB 3562 GAAATATTATTAATAATTTTATTTTATACAAAGTATTAACTAACCCATTAAACAGCTAAA 3621
QY 128 AGAGTTTTTTCACCTTTAAACATAGGCTATCCCACTGGTGGATACAGCAATT 180
DB 3622 AAAACAATCCTTAACACCTATATATATCCCATTTGCTTATTACGAGCTTTT 3674

RESULT 13
US-08-971-395-4/c
Sequence 4, Application US/08971395
Patent No. 6359197
GENERAL INFORMATION:
APPLICANT: Amasino, Richard M
APPLICANT: No. 6359197, Yoo-Sun
APPLICANT: Gan, Susheng
TITLE OF INVENTION: Transgenic Plants with Altered Senescence Characteristics
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
STATE: WI
COUNTRY: US
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/971,395
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 960296.94908
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000

TELEFAX: 608-251-9166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5303 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-971-395-4

Query Match 10.7%; Score 32.2; DB 4; Length 5303;
Best Local Similarity 52.6%; Pred. No. 3.3;
Matches 70; Conservative 0; Mismatches 63; Indels 0; Gaps 0;
Qy 4 TTTCAGGTCAATCATTCATTAGTTTCTAGTCTATTAACTGGGTTTCTTAGGTCAGG 63
Db 648 TTAACATATCTCAATAAATAAGTAAGGTATCATCTTTTGGGTGTTTCGTCATAAG 589
Qy 64 CATTATATTACTAACCTTATTGTTAAATATCTAACCATPAAGAAATTAACATAATGCT 123
Db 588 TAGTATTTTTTTGTAGAAATTTGATAATCTTAAACTAAAGATAATTAATATTTTAAAGT 529
Qy 124 GAATAGAGTTTTT 136
Db 528 ATATAAATTTGTAT 516

RESULT 14
US-08-844-274-11
; Sequence 11, Application US/08844274B
; Patent No. 6218185
; GENERAL INFORMATION:
; APPLICANT: Fraser Jr., Malcom J.
; APPLICANT: Shirk, Paul D.
; APPLICANT: Ellick, Teri A.
; APPLICANT: Perera, Omathage
; TITLE OF INVENTION: PiggyBac Transposon-Based Genetic Transformation System
; FILE REFERENCE: 0148.96
; CURRENT APPLICATION NUMBER: US/08/844,274B
; EARLIER APPLICATION NUMBER: 1997-04-18
; EARLIER FILING DATE: 1996-04-19
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0 - beta
; SEQ ID NO 11
; LENGTH: 2476
; TYPE: DNA
; ORGANISM: Trichoplusia ni
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (333)..(2123)
US-08-844-274-11

Query Match 10.7%; Score 32; DB 4; Length 2476;
Best Local Similarity 55.4%; Pred. No. 3;
Matches 62; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
Qy 16 AATCATCATAGTATTTTGTAGTCTATTAACTGGGTTTCTTAGGTCAGGCATTATTATTAC 75
Db 150 AAGTGTCACGTGATTTTGAACATATAACGCCGGGTGAGTCAAAATGACGCATGATTATCTT 209
Qy 76 TAACCTTATTGTTAATATTCTAACCATAAAGAAATTAATTAATGTTGAAT 127
Db 210 TTACGTGACTTTTAAAGATTAACTCATACGATAATTAATATTGTTATTTCAT 261

RESULT 15
US-09-586-719-11
; Sequence 11, Application US/09586719
; Patent No. 6294345
; GENERAL INFORMATION:
; APPLICANT: Zheng, Feng

; APPLICANT: Levin, Joshua Z.
; APPLICANT: Bauer, Michael W.
; TITLE OF INVENTION: Herbicide Target Genes and Methods.
; FILE REFERENCE: PB/5-30909A
; CURRENT APPLICATION NUMBER: US/09/586,719
; CURRENT FILING DATE: 2000-06-05
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 4198
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-586-719-11

Query Match 10.7%; Score 32; DB 4; Length 4198;
Best Local Similarity 51.4%; Pred. No. 3.5;
Matches 74; Conservative 0; Mismatches 70; Indels 0; Gaps 0;
Qy 4 TTTCAGGTCAATCATTCATTAGTTTCTAGTCTATTAACTGGGTTTCTTAGGTCAGG 63
Db 3601 TTTAAGAGAAATAAATATATGTTCTAGGTGGGTCAATTTAGCAACTATATATGATG 3660
Qy 64 CATTATATTACTAACCTTATTGTTAAATATCTAACCATAAAGAAATTAATGCT 123
Db 3661 GATTATATTCTCTTATGATTGAAAAATTTGCAAGTGAGAAAAACATCATGTTTCTTCT 3720
Qy 124 GAATAGAGTTTTTTCACATTTAACAT 147
Db 3721 AAGTTGTCCTCCAGTCCTCAAT 3744

Search completed: May 10, 2003, 17:06:22
Job time : 83 secs

GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model

Run on: May 10, 2003, 17:05:02 ; Search time 119 Seconds
(without alignments)
3132.870 Million cell updates/sec

Title: us-09-721-391-1

Perfect score: 300

Sequence: 1 tcatttgcaggtcaaatca.....agccaagacatgtgataac 300

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 783854 seqs, 621352466 residues

Total number of hits satisfying chosen parameters: 1567708

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*

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- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	219	73.0	546	9	US-10-053-886-1
3	219	73.0	546	9	US-09-814-357-10
4	219	73.0	552	9	US-10-053-886-16
5	68.6	22.9	320	9	US-10-053-886-7
6	40.8	13.6	7195	9	US-10-239-676-29
7	40	13.3	2041	10	US-09-834-975-959
8	38.6	12.9	4985	9	US-10-094-240-10
9	37	12.3	3996	9	US-10-087-464-42
10	36.6	12.2	113604	9	US-10-227-195A-1
11	36.6	12.2	113604	9	US-10-227-195A-2
12	36.4	12.1	380	10	US-09-969-373-85
13	36.4	12.1	380	10	US-09-969-373-86
14	36.4	12.1	15649	10	US-10-239-676-103
15	35.8	11.9	1200	10	US-09-887-576-772
16	35.8	11.9	2000	9	US-09-938-842A-3433
17	35.4	11.8	264	10	US-09-969-373-472
18	35.4	11.8	608	9	US-09-938-842A-3718
19	35.2	11.7	10957	9	US-10-125-540-555

20	35.2	11.7	10957	9	US-10-103-313-615	-Sequence 615, App
21	35.2	11.7	10957	10	US-09-764-870-555	Sequence 555, App
22	35.2	11.7	10957	10	US-09-764-853-903	Sequence 903, App
23	35.2	11.7	13217	9	US-10-125-540-556	Sequence 556, App
24	35.2	11.7	13217	9	US-10-103-313-616	Sequence 616, App
25	35.2	11.7	13217	10	US-09-764-870-556	Sequence 556, App
26	35.2	11.7	13217	10	US-09-764-853-904	Sequence 904, App
27	35.2	11.7	13220	9	US-10-125-540-554	Sequence 554, App
28	35.2	11.7	13220	9	US-10-103-313-614	Sequence 614, App
29	35.2	11.7	13220	10	US-09-764-870-554	Sequence 554, App
30	35.2	11.7	13220	10	US-09-764-853-902	Sequence 902, App
31	35.2	11.7	32249	9	US-09-860-670-260	Sequence 260, App
32	34.8	11.6	562	9	US-09-736-457-733	Sequence 733, App
33	34.8	11.6	562	9	US-09-902-941-733	Sequence 733, App
34	34.8	11.6	562	9	US-09-849-626-733	Sequence 733, App
35	34.8	11.6	562	9	US-10-017-754-733	Sequence 733, App
36	34.8	11.6	7906	9	US-10-239-676-97	Sequence 97, Appli
37	34.6	11.5	254	10	US-09-969-373-1027	Sequence 1027, Ap
38	34.6	11.5	2000	9	US-09-938-842A-4180	Sequence 4180, Ap
39	34.2	11.4	5917	9	US-10-087-464-9	Sequence 9, Appli
40	34	11.3	17431	9	US-10-072-349-247	Sequence 247, App
41	34	11.3	17431	10	US-09-764-855-247	Sequence 247, App
42	34	11.3	684973	10	US-09-263-959-1	Sequence 1, Appli
43	33.6	11.2	2000	9	US-09-938-842A-3423	Sequence 3423, Ap
44	33	11.0	145831	10	US-09-969-708-79	Sequence 79, Appl
45	33	11.0	145831	10	US-09-954-456-2116	Sequence 2116, Ap

ALIGNMENTS

RESULT 1
US-09-822-634-2
; Sequence 2, Application US/09822634
; Patent No. US20020150556A1
; GENERAL INFORMATION:
; APPLICANT: Vile, Richard G.
; APPLICANT: Harrington, Kevin
; APPLICANT: Bateman, Andrew
; APPLICANT: Murphy, Steven
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TISSUE
; TITLE OF INVENTION: SPECIFIC GENE REGULATION THERAPY
; FILE REFERENCE: 07039-289001
; CURRENT APPLICATION NUMBER: US/09/822,634
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 60/193,977
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 300
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-634-2

Query Match 100.0%; Score 300; DB 10; Length 300;
Best Local Similarity 100.0%; Pred. No. 1.4e+68;
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	TCATTTCGAAGTCGCAATCATCTAGTTTCTAGTCTATTAACTGGGTTCTCTAGGTC	60
DB	1	TCATTTCGAAGTCGCAATCATCTAGTTTCTAGTCTATTAACTGGGTTCTCTAGGTC	60
QY	61	AGGCATTATTATTACTAACTTTATTGTTAATATCTTAACCAATAAGAAATTAATAAT	120
DB	61	AGGCATTATTATTACTAACTTTATTGTTAATATCTTAACCAATAAGAAATTAATAAT	120
QY	121	GCTGAATAGAGTTTTTCACTTTTAACATAGGCCCTATCCCACTGGTGGGATACAGCAAT	180
DB	121	GCTGAATAGAGTTTTTCACTTTTAACATAGGCCCTATCCCACTGGTGGGATACAGCAAT	180
QY	181	CGAAGAAAGTCAGTCATGCTCTTTTCAGAGGATGAAGCTTAGATATAAGACTAAAG	240

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Db 181 CGAAGAAAAGTCAGTCATGTCCTTTTCAGAGGATGAAGCTTAAGATAAAGACTAAAG 240
Qy 241 TGTTCATCGGAGTGGAGTGGTATTATATAGTCTCAGCCCAAGACATGCTGATAATC 300
Db 241 TGTTCATCGGAGTGGAGTGGTATTATATAGTCTCAGCCCAAGACATGCTGATAATC 300

RESULT 2
US-10-053-886-1
; Sequence 1, Application US/10053886
; Publication No. US20030039633A1
; GENERAL INFORMATION:
; APPLICANT: De-Chao Yu
; APPLICANT: Yuanhao Yu
; TITLE OF INVENTION: Recombinant Oncolytic Adenovirus for
; FILE REFERENCE: CELL-021
; CURRENT APPLICATION NUMBER: US/10/053,886
; CURRENT FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 09/814,357
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/192,015
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 09/814,351
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/192,156
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 546
; TYPE: DNA
; ORGANISM: H. sapiens
US-10-053-886-1

Query Match 73.0%; Score 219; DB 9; Length 546;
Best Local Similarity 99.6%; Pred. No. 1.9e-47;
Matches 230; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 71 ATTACTAACCTTATTGTTAAATATTCTAACCATAGAATAAATACTATTATGTTGAATAGA 130
Db 251 ATTACTAACCTTATTGTTAAATATTCTAACCATAGAATAAATACTATTATGTTGAATAGA 310
Qy 131 GTTTTTCACCTTTAACAATAGGCTATCCCACTGGTGGGATACGAGCAATTCGAAAG-AAA 189
Db 311 GTTTTTCACCTTTAACAATAGGCTATCCCACTGGTGGGATACGAGCAATTCGAAAGAAA 370
Qy 190 AGTCAGTCATGTCGCTTTTCAGAGGATGAAGCTTAAGATAAAGACTAAAGTGTGTTGATG 249
Db 371 AGTCAGTCATGTCGCTTTTCAGAGGATGAAGCTTAAGATAAAGACTAAAGTGTGTTGATG 430
Qy 250 CTGGAGTGGGAGTGGTATTATATAGTCTCAGCCCAAGACATGCTGATAATC 300
Db 431 CTGGAGTGGGAGTGGTATTATATAGTCTCAGCCCAAGACATGCTGATAATC 481

RESULT 3
US-09-814-357-10
; Sequence 10, Application US/09814357
; Publication No. US20030068307A1
; GENERAL INFORMATION:
; APPLICANT: Yu, De-Chao
; APPLICANT: Chen, Yu
; TITLE OF INVENTION: METHODS OF TREATING NEOPLASIA
; TITLE OF INVENTION: WITH COMBINATION TARGET CELL-SPECIFIC ADENOVIRUS,
; FILE REFERENCE: 348022001600
; CURRENT APPLICATION NUMBER: US/09/814,357
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 60/192,015
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 35
```

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 546
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Tyrosinase-TRE
US-09-814-357-10

Query Match 73.0%; Score 219; DB 9; Length 546;
Best Local Similarity 99.6%; Pred. No. 1.9e-47;
Matches 230; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 71 ATTACTAACCTTATTGTTAAATATTCTAACCATAGAATAAATACTATTATGTTGAATAGA 130
Db 251 ATTACTAACCTTATTGTTAAATATTCTAACCATAGAATAAATACTATTATGTTGAATAGA 310
Qy 131 GTTTTTCACCTTTAACAATAGGCTATCCCACTGGTGGGATACGAGCAATTCGAAAG-AAA 189
Db 311 GTTTTTCACCTTTAACAATAGGCTATCCCACTGGTGGGATACGAGCAATTCGAAAGAAA 370
Qy 190 AGTCAGTCATGTCGCTTTTCAGAGGATGAAGCTTAAGATAAAGACTAAAGTGTGTTGATG 249
Db 371 AGTCAGTCATGTCGCTTTTCAGAGGATGAAGCTTAAGATAAAGACTAAAGTGTGTTGATG 430
Qy 250 CTGGAGTGGGAGTGGTATTATATAGTCTCAGCCCAAGACATGCTGATAATC 300
Db 431 CTGGAGTGGGAGTGGTATTATATAGTCTCAGCCCAAGACATGCTGATAATC 481

RESULT 4
US-10-053-886-16
; Sequence 16, Application US/10053886
; Publication No. US20030039633A1
; GENERAL INFORMATION:
; APPLICANT: De-Chao Yu
; APPLICANT: Yuanhao Yu
; TITLE OF INVENTION: Recombinant Oncolytic Adenovirus for
; FILE REFERENCE: CELL-021
; CURRENT APPLICATION NUMBER: US/10/053,886
; CURRENT FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 09/814,357
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/192,015
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 09/814,351
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/192,156
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 552
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(6)
; OTHER INFORMATION: AgeI restriction site
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (547)...(552)
; OTHER INFORMATION: AgeI restriction site
US-10-053-886-16

Query Match 73.0%; Score 219; DB 9; Length 552;
Best Local Similarity 99.6%; Pred. No. 2e-47;
Matches 230; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 71 ATTACTAACCTTATTGTTAAATATTCTAACCATAGAATAAATACTATTATGTTGAATAGA 130
Db 252 ATTACTAACCTTATTGTTAAATATTCTAACCATAGAATAAATACTATTATGTTGAATAGA 311
```


SEQ ID NO 959
LENGTH: 2041
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(2041)
OTHER INFORMATION: n = A,T,C or G
US-09-834-975-959

Query Match 13.3% Score 40; DB 10; Length 2041;
Best Local Similarity 100.0%; Pred. No. 0.98;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 261 AGTGGTATTATATAGGCTCAGCCACACATGTGATATC 300
|||||
Db 7 AGTGGTATTATATAGGCTCAGCCACACATGTGATATC 46

RESULT 8

US-10-094-240-10
Sequence 10, Application US/10094240
Publication No. US20030082637A1
GENERAL INFORMATION:
APPLICANT: ZWIEBEL, LAURENCE J.
TITLE OF INVENTION: ARRESTIN GENE, POLYPEPTIDE, AND METHODS OF USE THEREOF
FILE REFERENCE: N8289
CURRENT APPLICATION NUMBER: US/10/094,240
CURRENT FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: 10/056,405
PRIOR FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: 60/264,649
PRIOR FILING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn ver. 2.1
SEQ ID NO 10
LENGTH: 4985
TYPE: DNA
ORGANISM: Anopheles gambiae
US-10-094-240-10

Query Match 12.9% Score 38.6; DB 9; Length 4985;
Best Local Similarity 56.8%; Pred. No. 3.3;
Matches 71; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

Qy 17 ATCATCATAGTTTGTAGTCTATTAACTGGTTTGGTTAGTCAGGCATTATTATTACT 76
|||||
Db 2561 ATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATT 2620

Qy 77 AACCTTATTGTTAATATCTCAACCATAGAATTAACCTAATTAATGGTGAATAGAGTTTTT 136
|||||
Db 2621 ATTATTATTATTATTATTATAACAATAATAATTATTATTATTATTATTATTATTATT 2680

Qy 137 CACTT 141
|||
Db 2681 AATTT 2685

RESULT 9

US-10-087-464-42/C
Sequence 42, Application US/10087464
Publication No. US20030059436A1
GENERAL INFORMATION:
APPLICANT: Chishti, Athar
APPLICANT: Oh, Steven
APPLICANT: Liu, David
APPLICANT: Goel, Vikas
APPLICANT: Li, Xuerong
TITLE OF INVENTION: Band 3 Antigenic Peptides, Malaria Polypeptides and Uses Thereof
FILE REFERENCE: S1237/7019
CURRENT APPLICATION NUMBER: US/10/087,464
CURRENT FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 06/272,930

PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 59
SOFTWARE: PatentIn version 3.0
SEQ ID NO 42
LENGTH: 3996
TYPE: DNA
ORGANISM: Plasmodium falciparum
US-10-087-464-42

Query Match 12.3% Score 37; DB 9; Length 3996;
Best Local Similarity 54.9%; Pred. No. 7.8;
Matches 73; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

Qy 15 AATCATCATAGTTTGTAGTCTATTAACTGGTTTGGTTAGTCAGGCATTATTATTA 74
|||||
Db 3647 ACATTTTCATTATTATCAACTGAAATATCATTTTAAATTCATTTTCAGAA 3588
|||||

Qy 75 CTAACCTTATTGTTAATATCTCAACCATAGAATTAACCTAATTAATGGTGAATAGAGTTT 134
|||||
Db 3587 TTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATGCT 3528
|||||

Qy 135 TTCACCTTTAACAT 147
|||||
Db 3527 TTCACCTTTATAT 3515
|||||

RESULT 10

US-10-227-195A-1/c
Sequence 1, Application US/10227195A
Publication No. US20030077633A1
GENERAL INFORMATION:
APPLICANT: Cox, David
APPLICANT: Arnold, Deana
TITLE OF INVENTION: Haplotype structure of chromosome 21
FILE REFERENCE: 1030U1
CURRENT APPLICATION NUMBER: US/10/227,195A
CURRENT FILING DATE: 2002-11-18
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 113604
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: 7175, 7204, 36973, 66372, 76921, 81512, 88727
OTHER INFORMATION: n = G or C
US-10-227-195A-1

Query Match 12.2% Score 36.6; DB 9; Length 113604;
Best Local Similarity 52.3%; Pred. No. 41;
Matches 81; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

Qy 1 TCATTTGCAAGTCAAATCATCATTAGTTTGTAGTCTATTAACTGGTTTGGTTAGTCT 60
|||||
Db 17349 TAACCTGGCTGGTATTAATGCATATTTTGTAGTCTTTAACTGACTGGTACATTTT 17290
|||||

Qy 61 AGGCATTATTATTACTAACCTTATTGTTAATTTCTTAACCATAGAATTAACCTAAT 120
|||||
Db 17289 ATTCACTTTTTTACAAATCCATGATTTGTACACAGATAAAATTTAAATGGCAGAGAAAT 17230
|||||

Qy 121 GGTCAATAGAGTTTTTTCACCTTTAACATAGGCCTAT 155
|||||
Db 17229 TATATATACACTTTTGATATTTATATATGATGT 17195.
|||||

RESULT 11

US-10-227-195A-2/c
Sequence 2, Application US/10227195A
Publication No. US20030077633A1
GENERAL INFORMATION:
APPLICANT: Cox, David
APPLICANT: Arnold, Deana

; TITLE OF INVENTION: Haplotype structure of chromosome 21
; FILE REFERENCE: 103001
; CURRENT APPLICATION NUMBER: US/10/227,195A
; CURRENT FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 113604
; TYPE: DNA
; ORGANISM: Human
US-10-227-195A-2

Query Match 12.2%; Score 36.6; DB 9; Length 113604;
Best Local Similarity 52.3%; Pred. No. 41;
Matches 81; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

QY 1 TCATTGCAAGGTCAAATCATCTATTAGTTTGTAGCTATTAACTGGGTTGGCTTAGGTC 60
DB 17349 TAACCTGGCTGGTATTATGATATTTTGTAGCTTTTAACTGACTGCGTACATTTT 17290
QY 61 AGGCATTATTACTAAACCTTATTGTTAATATTCTAACCATAAGAAATTAACCTATTAAT 120
DB 17289 ATTCACTTTTTCACATCCATGTTTACACAGTAAATAATTTAAATGCGCAGAAAT 17230
QY 121 GGTGATAGAGTTTTCACCTTTTAACTAGGCCTAT 155
DB 17229 TATATATACACTTTTCATATTTATATATATGCGTGT 17195

RESULT 12
US-09-969-373-85
; Sequence 85, Application US/09969373
; Patent No. US20020133852A1
; GENERAL INFORMATION:
; APPLICANT: Effertz, Roger J.
; APPLICANT: Hauge, Brian M.
; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
; FILE REFERENCE: 38-10(52679)A
; CURRENT APPLICATION NUMBER: US/09/969,373
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 09/754,853
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 09/760,427
; PRIOR FILING DATE: 2001-01-13
; PRIOR APPLICATION NUMBER: US 09/855,768
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 4593
; SEQ ID NO 85
; LENGTH: 380
; TYPE: DNA
; ORGANISM: Glycine max
US-09-969-373-85

Query Match 12.1%; Score 36.4; DB 10; Length 380;
Best Local Similarity 54.5%; Pred. No. 4.1;
Matches 73; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 65 ATTATTACTAACCTTATTGTTAATATTCTAACCATAAGAAATTAACCTATTAAATGGTG 124
DB 212 ATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATT 271
QY 125 AATAGAGTTTTCACCTTTAACATAGCCCTATCCACTGGTGGGATACGACCAATTCGAA 184
DB 272 ATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATT 331
QY 185 AGAAAGTCAGTCA 198
DB 332 AGAACATAAATGA 345

RESULT 13
US-09-969-373-86
; Sequence 86, Application US/09969373

; Patent No. US20020133852A1
; GENERAL INFORMATION:
; APPLICANT: Effertz, Roger J.
; APPLICANT: Hauge, Brian M.
; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
; FILE REFERENCE: 38-10(52679)A
; CURRENT APPLICATION NUMBER: US/09/969,373
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 09/754,853
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 09/760,427
; PRIOR FILING DATE: 2001-01-13
; PRIOR APPLICATION NUMBER: US 09/855,768
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 4593
; SEQ ID NO 86
; LENGTH: 380
; TYPE: DNA
; ORGANISM: Glycine max
US-09-969-373-86

Query Match 12.1%; Score 36.4; DB 10; Length 380;
Best Local Similarity 54.5%; Pred. No. 4.1;
Matches 73; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 65 ATTATTACTAACCTTATTGTTAATATTCTAACCATAAGAAATTAACCTATTAAATGGTG 124
DB 212 ATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATT 271
QY 125 AATAGAGTTTTCACCTTTAACATAGCCCTATCCACTGGTGGGATACGACCAATTCGAA 184
DB 272 ATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATT 331
QY 185 AGAAAGTCAGTCA 198
DB 332 AGAACATAAATGA 345

RESULT 14
US-10-239-676-103
; Sequence 103, Application US/10239676
; Publication No. US20030082609A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with Gene Regulation
; FILE REFERENCE: 5013.1003
; CURRENT APPLICATION NUMBER: US/10/239,676
; CURRENT FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: PCT/EP01/03968
; DE 10019058.8
; DE 10019173.8
; DE 10032529.7
; DE 10043826.1
; PRIOR FILING DATE: 2001-04-06
; 2000-04-06
; 2000-04-07
; 2000-06-30
; 2000-09-01
; NUMBER OF SEQ ID NOS: 228
; SEQ ID NO 103
; LENGTH: 15649
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-239-676-103

Query Match 12.1%; Score 36.4; DB 9; Length 15649;
Best Local Similarity 56.8%; Pred. No. 20;
Matches 67; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

